











Qy 346 SerArgProGlyLysIleThrArgLys-----ThrIleMetMetAsnThrArg 362  
 Db 2191 AGTCGCCAGCAGCCGCTGATCCTAGTGGTCCCACCGCCCTGGACACATCC 2250

Qy 363 -----MetArgGluLeuGluLeuLysGluArgSerSerLysSer 375  
 Db 2251 TCCGAGGGAAACAGATACTCTCCGCTGAGCTGAAGAGGTCTCGAAATCG 2310

Qy 376 LeuLeuAlaAsnValleAspIleAspAspPheArgHisGly-----ProProPro 393  
 Db 2311 CTGCCTGCCAACGTACTAGACATCGATGATACTTCGGCACAAATTGGTGCCTCCATGACG 2370

Qy 394 ProAsnSerThrAlaserThrGlyAsnLeuGlyProGlyCysSerIlePheArgThrAsp 413  
 Db 2371 CCCGGC-----GGAACATGCCCCACACAAACCCGGCTTTCTATCGCAAGGTT 2415

Qy 414 PheArgArgSerPheValArgProSerThrMetGluAspValGly-----GlyGlyLeu 431  
 Db 2416 TATGGCAAGGC-----GACGATGGCNCATGGGCCATT 2451

Qy 432 GlySer-----HishisArg----- 436  
 Db 2452 GGCAGCCTCCATGGGATGGGTACCCATCATAGTCATCAAATCATCAAATGAA 2511

Qy 437 ---GluLeuHisLeuIleLeuArgGluLeuGlnPheIleThrAlaArgMetLysAla 455  
 Db 2512 TATGAAATTAGCTTTAACCTTAAGGAAATTGGCTTTAACATGATGAGCTAACGAT 2571

Qy 456 AspGluGluAlaGluLeuIleSerAspTrpIlysPheAlaAlaMetValValAspArgPhe 475  
 Db 2572 GACGAGTGCAATGACAATGGCAATGATTTGAGAATTTCAGCTATGGCTGTGACACCTG 2631

Qy 476 CysLeuPheValPheThrIleAlaThrValAlaValLeuSerAla 495  
 Db 2632 TGCCATTATCATATTACAAATGGTCCGATAATTAGCTTAACTACTATCAGCA 2691

Qy 496 ProHisIleIleVal 500  
 Db 2692 CCACATATTATTGTC 2706

Search completed: May 9, 2004, 00:55:43  
 Job time : 5552.12 secs

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OM protein - nucleic search, using frame\_pplus\_p2n model

Run on: May 8, 2004, 06:39:04 ; Search time 526.234 Seconds  
 Perfect score: 4044.486 Million cell updates/sec  
 Sequence: 1 MAPMMAALLALIPLLIVSEQQ . . . . . LFTIATAVILSAPHILVQ 501

Title: US-09-303-232-6  
 Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Rgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Command line parameters:

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-Q-/cgm2.1/usr/spool/cgm2/runat 07052004_101109_23873/app query .fasta_1.22261
-DB=N Geneseq_29Jan04 -QFMT=fasta -SUFFIX=rng -MINMATCH=0,1,-LOOPCFL=0
-LCOPENR=0 -UNITS=bits -START=1 -END=1 -MATRIX=blossom62 -TRANS=human40.odi
-LIST=45 -DOALIGN=200 -THR SCOREB=PCT -THR MAX=1.00 -THR MIN=0 -ALIGN=15
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-NO_MMW -LARGEQUERY -NEG SCORE=0 -BLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADD=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DELEXT=7
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Database : N Geneseq\_29Jan04:  
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 2: geneseqn1990s:  
 3: geneseqn2000s:  
 4: geneseqn2001s:  
 5: geneseqn200198s:  
 6: geneseqn2002s:  
 7: geneseqn2003s:  
 8: geneseqn2003bs:  
 9: geneseqn2003cs:  
 10: geneseqn2004s:  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID Description

1	2640	100.0	3109	3	AZ24477	Aat24477 H. viresc
2	1968	74.5	1540	4	ABLO7231	Abi07231 Drosophili
3	1803	68.3	3700	3	Aazz24476	Aaz24476 H. viresc
4	1669	60.9	2886	3	Aazz24475	Aaz24475 D. melano
5	1283	48.6	936	4	ABL13733	Abi13733 Drosophili
6	1258	47.7	1509	3	AAC51395	Aac51395 Human PRO
7	1258	47.7	1509	4	AAC50380	Aac50380 Wild-type
8	1258	47.7	1876	2	AAV12197	AAV12197 Human neu

Summaries

Alignments

Result 1  
 AA224477 standard; cDNA to mRNA; 3109 BP.  
 ID XX  
 AC XX  
 AA224477;  
 XX DT 17-FEB-2000 (first entry)  
 XX DE H. virescens acetyl-choline receptor DNA from clone Hva7-2.  
 XX KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;  
 KW neurotransmission; plant protection agent; conductance; AChR; ds.  
 XX KW Heliothis virescens.  
 XX OS  
 PN DE19819829-A1.  
 XX PD 11-NOV-1999.  
 XX PP 04-MAY-1998; 98DE-01019829.  
 XX PR 04-MAY-1998; 98DE-01019829.  
 XX PR (PARB ) BAYER AG.  
 XX PI Adamczewski M., Oellers N., schulte T;  
 XX DR WBI, 2000-014207/02.  
 DR P-PSDB; AAV50816.  
 PT New nucleic acid encoding a nicotinic acetylcholine receptor from  
 PT insects, used to identify potential insecticides.



PN	WO200171042-A2.	Qy	136 LeuTyValProProGlyIlePheIysSerThrCysLysMetAspIleAlaAlaTrpPhePro
XX	27-SEP-2001.	Db	470 CTGACGTGCCCTGGTATCTCAAGAACATCAAGATAGAACATCC 529
PD		Qy	156 PheAspAspGlnHscysAspMetLysPheGlySerTrpIhrTyaspGlyAsnLeu 175
XX	23-MAR-2001; 2001WO-US009231.	Db	530 TTTGTGACCAACATGCAAATGGTAGTTGACTAGATGGAAATCGATTAGATGGAAATCGATTG 589
PF		Qy	176 AspLeuValIleLysAspGluIaGlyIysAspIleLeuIhrArgIysGlu 195
XX	23-MAR-2000; 2000US-0191637P.	Db	590 GATTGGTTGAAAGTCCGAAGTGGGGATCTTCGATTICATAAAATGCGAG 649
PR	11-JUL-2000; 2000US-00614150.	Qy	
XX	(PEKE ) PE CORP NY.	Db	
XX	Venter JC, Adams M, Li PWJ, Myers EW;	Qy	196 TrpTrpLeuIleGly----MetProGlyIysAsnThrIleIhrTyAlaCysCysPr 214
XX	WPT; 2001-656860/75.	Db	650 TGGTACTGCTTGTGTTACATTGCGCCCTCTGCC 709
DR	P-PSDB; ABB63128.	Qy	214 oGluProTyvalAspValThrPheThrIleMetIleGargArg9ThrLeuItyTrp 234
XX	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.	Db	710 AGAACATATGTCGATATACCCRATACATAAAATCTGCCTGATCATTAATT 769
PS	SEQ ID NO 16175; 21PP + Sequence Listing; English.	Qy	234 ephA5LeuIleValProCysValLeuIleSerIleMetIleGlyLeuIleGlyThrIle 254
XX	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL0180-ABL6175) and the encoded proteins (ABB57737-AB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at <a href="ftp://wipo.int/pdb/published_pct_sequences">ftp://wipo.int/pdb/published_pct_sequences</a>	Db	770 TTTCATTTAATTGCCCATTGTCATACTCGATGGCCCTACTGGCTTCACATT 829
CC		Qy	254 uprobroAspSerGlyGluIysIleThrLeuIleSerIleThrLeuIle 274
CC		Db	830 GCCCGGAAATTCCGGGAAACTGACGTGGGAAATATACTATCACATCACAGT 889
CC		Qy	274 1pheLeuasnLeuValAlaGluThrLeuProGlnValSerAspAlaIleProLeuIeG 294
CC		Db	890 ATTCATAACCTTGCGGAAATGCGATGCGGAAACGTCGGATGTCATGCTTCATAGG 949
CC		Qy	294 YThr----- 295
XX	Sequence 1540 BP; 412 A; 390 C; 376 G; 362 T; 0 U; 0 Other;	Db	950 TACACACAGATATTAAAAGCTATAGCTTAAAGTAGCGGACGATGGTGGACTAT 1008
SQ		Qy	296 -----TyrPheAsnCysIleMetPheMetVa 304
Alignment Scores:		Db	1009 CGACCACTACTACCGTGTGCGACAGAAAGCACTACTCAATGCAATGTCATGGT 1068
Pred. No. :	1.11e-200	Length:	344 ehisGluMetProGlnTrpIleSerValPheIleGlnTrpIleProPheIleVal 344
Score:	1968.00	Matches:	Db 1129 TCAGGAGATGCCACCGTGATCGTGTCTTCTACATGCTGCGCTCG 1188
Percent Similarity:	82.19%	Conservative:	Qy 304 IAlaSerSerIleValIleUthValValLeuAsnTyRHisIArgThrAlaAspD 324
Best Local Similarity:	74.95%	Mismatches:	Db 1069 CGCTCGTGGTGTGTGTGACAGTAGTGCTCAATACCACATCCACCGGACAT 1128
Query Match:	74.55%	Indels:	Qy 324 ehisGluMetProGlnTrpIleSerValPheIleGlnTrpIleProPheIleVal 344
DB:	4	Gaps:	Db 1189 ATGGCTGACCCGGTCCGATTCACGCAAAACCATACTAACATGCTGAA 1248
US-09-303-232-6 (1-501) x ABL07231 (1-1540)		Qy 364 gGluLeuIleLeuIysGluArgSerIleSerIleLeuAlaAsnValLeuAspIleAs 384	
Qy	2 AlatrometLeuAlaAlaLeuAlaLeu-----LeuAlaLeuLeuPro 15	Db 1249 GGCTGGAGTAAAGGGCTCTCCAAATCCCTGTGGCAATGCTCGATCATG 1308	
Db	50 TCCCGCTTCAGGCTGCTGTCCTGTTCTGTTGATCTTCTCGATAATAAA 109	Qy 384 pAspAspPheArgHisGlyProProProAsnSerThrAlaSerThrGlyAsnLeuG 404	
Qy	16 ValSerGluGlnGlyProHisGluIysArgLeuIleAsnIleLeuAsnTyAsn 35	Db 1309 CGCGACTTCGGCAC 1347	
Db	110 GAAAGCTGCAAGGACCTATGAAAAGCCCTGCTGTGACCATCTGCCTCCCTACAT 169	Qy 404 yProGlyCysSerIlePheArgArgSerPheValArgProserThrMe 424	
Qy	36 ThrLeuGluIargProValAlaAsnGluSerGluProLeuIargPheGlyLeuThr 55	Db 1348 CATTGGCTCGTG-----GCGACTCTGCCACAAAGCT 1386	
Db	170 ACGGTGGAGGCCGTSGCCAATGATGGAGGCCCTGAGGTAAAGTCGAACAGC 229	Qy 424 tGluAspValGlyGlyLeuGlySerHisIArgLeuIleLeuIleLeuArgG 444	
Qy	56 LeuGlnGlnIleAspValAspGluIysAsnGlnIleLeuIleThrAsnIleTrpLeu 75	Db 1387 GGAGGAGATCACCGCCACATGGCTGCAATACAAGATCTCACTAAAG 1446	
Db	230 CTGAGCAAGATCATCGACCTGGATGAAAGAAATCGATTCGTTGTTA 289	Qy 444 uLeuGlnPheIleThrAlaArgMetLysIleAspDgluGluAlaGluLeuIleSerS 464	
Qy	76 SerIleGluItrpAsnAspTyRAsnLeuIgTpaNAspSerGluTyGlyGlyVallys 95	Db 1447 ATTCAAATTAACTACCGCAGTGGCAAACTGAGCTTCATCTCAAACT 1506	
Db	290 AATTGGACTGGACGACTACATCTGCTGCTGAAATGAAACGAAATCGGCCGTGAA 349	Qy 464 pTrpLySpheAlaAlaMetValValAspArg 474	
Qy	96 AspLeuArgIleThrProAlnIysLeutrpIlyProAspValIeuMetTyAsnSerAla 115		
Db	350 GATCTACGAATCACGCCAACAGCTGTTGAAAGCCGACGTGTCATGACACAGCG 409		
Qy	116 AspGluGlyPheAspGlyIysLeutrpIlyProAspValIeuMetTyAsnSerAla 135		
Db	410 GATGAGGATTCGATGGCAAGCTGAGCAGTGGCAAACTGAGCTTCATCTCAAACT 469		

Db	1507	tTcGAAGTTGCGCCAATGTGATGG	1537
QY	41	VALALAASNGLUSERGLUPROLEUGLUVALARGLYLEUTHRLLEUGINGNINILE	60
Db	488	GTCGTCAACGAGCACCCTCATGCCTCATGAGATAC	547
QY	61	ASPVALAPGLULYSARGLNLEUERLEUASNILETRIPLEUSERIENGLURPASN	80
Db	548	GACGTGGAGAGAACAGCTGGCTTAACTAGAGTCGAAAT	607
QY	81	ASPTYRAASNLLEAARGTRDASNAPSERGLUTYRGLYGLIVALLYASPLEAARGLIEHLHR	100
Db	608	GATATGACTTGAGGGACACTAGATTGCGGGCTCAAGATTAAAGTGGCCA	667
QY	101	PROASMLYSLEUTRPLYSPROASPVALLUEUMETYRASPERSERALAAASPGIUGLYPHASP	120
Db	668	CCCCACAGACTATCGAAACAGACTGCTTATGTACAACAGGCCGACAGGGTTCGAC	727
QY	121	GLYTHRITYGLNTHASNVAVLVAVLAASGRLYGLYSERCVLEUTRYVALPPOPRO	140
Db	728	AGCACGTATCCAAAGAACAGGGCTGGCTGAGCTGTCGACGTGCCGCC	787
QY	141	GLYLEPHELYSSERTHRCYSLYSMETASPILEALATRPHEPRTHEPROTHEASPGLINHIS	160
Db	788	GGCATCTTAAGACACCCGCAAGATGACATCACCTGGATCAGTGGACCCACGAA	847
QY	161	CYSASPMETLYSPEGLYSSERTPPTHRTRYTASPGLYASNGINLEUASPLAUYLEU	180
Db	848	TGCGCAGATGAAAGTTGGCGACTGTGCACTTATGATGETATCAGTGTCAAATACAG	907
QY	181	ASPGLUAIALGGLYASPLEUASPERPHILERHASNGLYGLUTRPTYRLEUILEGY	200
Db	908	GATGCAAGGGGGCGAGGATAAAAGCAGTTGTCAGAATGGGAATGGGAGCTTAAATAGGA	967
QY	201	METPROGLYLYSSAASNTHRILETHRILYRACYSCYSPROGLUPROTYVALASPVAL	220
Db	968	GRCGCCGGAAGGCCAACGAGATCTAAACTGTTGTCGGGCCATCATGCACATC	1027
QY	221	THRPHETHRILEMELTILEARGARGLYRLEUTYTRYTYPHEASNLLEUVALPRO	240
Db	1028	ACGTTTGGCTGGATCCTGGCATCCGGAGAAAACCTCTACTACTCTCATGTCATGRCGCC	1087
QY	241	CYSVALLEUILLSERMNETALAELEUENGLYPHATHRLIEUPROPROASPSEGYGLU	260
Db	1088	TGGCTGCTCATGGCCTCATGGCCTCATGGCCTATGGGTRICACTTGGCTCAGACTC	1147
QY	261	LYSLEUTHRILEUGLYVALTHRILEULEASELTHRVPHELAEUASNLEUVALALA	280
Db	1148	AAGTTGCTTAGGTGAGATAATACGCGTCAATGGGTCACATGGGCG	1207
QY	281	GLUTHRLEUProGlnValSerAspAlaIleProLeuGlyThrTyrPheAsnCysIle	300
Db	1208	GAGAGGATGCGACGGGACGTCGACGGGTCACCTACTTCACACTGCACTGCATC	1267
QY	301	METHIEMETVALAIASERVALSERVALVALVALAASNNTYHISIARG	320
Db	1268	ATGTTCATGGTGGTCCCTCGTCGTCACCATCATGTCCTCAACTACCAACCGG	1327
QY	321	THRALAASPLIEHISGLUMETPROGLNPROLEUPLYSERVALPHELEUGLNTRPLEURO	340
Db	1328	CACCGAGACATCAAGAAATGAGTGAATGTCGTCCTATGGCTCCG	1387
QY	341	TRPYLEUURGMEESERARGPROGLYLYSYL16THRAGLYSTHRILEMetMetAsn	360
Db	1388	TGGGTTGCTGGCATCTCACGCCGCCCTCGCGACGACAGGCCGCCGGCGCGCT	1444
QY	361	THRARGMETHARGSERLYSSELERLSELAALASVNAVALAASVNAVALA	380
Db	1445	CCTCCGGCCGGCGACCTGGAGCTGGCTGGCGAGGGGGACCTCTGG	1504
QY	381	LEUASPILEASPADSPASPFEEARGHISGLYPROPROPROProAsnSerThrAlaSerThr	400
Db	1505	CTCGAATCTAGCAACTTCGCCAC-----CCGCAAGGCCAGCAG-----	1546





QY 184 GlyGlyAspLeuSerAspIleThrAsnGlyGlutDtryLeuIleGlyMetProGly 203  
 DB 598 GGTGGCAATTCCTAGCTTATAACCAAGGGAATGGGACTTTAATGGTGCCGCT 657

QY 204 LysLysAsnThrIleThrAlaCysCysProGluProGlyValAlaThrPheThr 223  
 DB 658 AACGAAATTAACTTACATAATTGCTGCCAGAACCTTAATGACTAACTTCGCGC 717

QY 224 IleMetIleArgArgGlnLeuTyrrTyrrPheAsnIleIleValProGly 243  
 DB 718 ATTGTGATTAAGCGAAAAAGTTGACTATTTCACACTGATTTCAACCTGTTACTG 777

QY 244 IleSerSerMetAlaLeuIleGlyPheThrLeuProProAspSerGlyGlyLeuThr 263  
 DB 778 ATCGCTCATGGACTGCTAGGGTTAACGTGACCAGATTCGGTAAAGCTTGG 837

QY 264 LeuGlyValThrIleLeuSerIleIleValAlaGluThrLeu 283  
 DB 838 CTTGAGTACAATTCTATTCGTTAACATGGTCTAACATGGTGCCTCAAACAAATG 897

QY 284 ProGlnValAspAspAlaIleProLeuLeuGly 294  
 DB 898 CCGCGACCTCCGATGGGTTACCGCTGCTCGGT 930

## RESULT 6

ID AAC58395 standard; cDNA; 1509 BP.

XX AAC58395;

XX 29-JAN-2001 (first entry)

XX Human PRO2145 nucleotide sequence SEQ ID NO:76.

XX DE Homo sapiens.

XX WO2000033755-A2.

XX 14-SEP-2000.

XX 05-JAN-2000; 2000WO-US000376.

XX 08-MAR-1999; 99WO-US005028.

PR 02-JUN-1999; 99WO-US012254.

PR 23-JUN-1999; 99US-014103P.

PR 07-JUL-1999; 99US-014104P.

PR 26-JUL-1999; 99US-014569P.

PR 30-NOV-1999; 99WO-US028313.

PR 20-DEC-1999; 99WO-US030911.

PR 05-JAN-2000; 2000WO-US000219.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillian KJ, Roy MA;

PI Watanabe CK, Wood WI;

XX DR WPI: 2000-572270/53.

DR P-PSDB; AAB24088.

XX Thirty PRO polymucleotides encoding PRO polypeptides, useful in the

XX treatment, diagnosis and prevention of cancer.

PS Claim 50; FIG 57; 286PP; English.

XX The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO12, PRO290, PRO943, PRO1005, PRO1009, PRO117, PRO809, PRO830, PRO848, PRO947, PRO1107, PRO1111, PRO1157, PRO1182, PRO1184, PRO1187, PRO1030, PRO1097, PRO1107, PRO1111, PRO1157, PRO1182, PRO1184, PRO1187, PRO1198. PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds may be used to treat various conditions including those characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytic, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AAC58366 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC58367 to AAC58396 and AAB24087 to AAB24089 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention

XX SQ Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 U; 0 Other;

XX Alignment Scores:  
 Pred. No.: 8 LeuAlaLeuLeuIa---LeuIeuProValSerGluGlnGlyProHisGluLysArgLeu 26  
 Score: 1.46e-124 Length: 1509  
 Percent Similarity: 1258/150 Matches: 150  
 Best Local Similarity: 63.23% Conservative: 75  
 CC Qy 28 CTGGCTCTGGCCGGCTGCTGCACTGTCCCTGCAAGGGCAGTTCCAGAGAACCTT 87  
 CC DB 27 LeuAsnAlaLeuLeuAlaAsnTyrrTyrAsnThrLeuGluArgProValAlaAsnGluSerGlu 46  
 CC DB 88 TACAGGAGCTGCTGAGAACATCACATCCCTGAGGCCAGCCCTGCCATGACTCGCA 147  
 CC Qy 47 ProLeuGluIvalArgPheGlyLeuThrIleLeuAspValAspGluIlyAsn 66  
 CC DB 148 CCACTCACCGCTACTTCCTGAGCTCCCTGAGATCATGACGTCGATGAGAAGAC 207  
 CC Qy 67 GluLeuIeuIleThrAspIleTrpLeuSerLeuGluTrpAsnAspIleArgTrp 86  
 CC DB 208 CAAGTAAACCAACATTGGCTGAAATGCTGGCATGATCACTATTACGTRGG 267  
 CC Qy 87 AsnAspSerGluTyrrGlyGlyWallyAspLeuArgIleThrProAsnLysLeuTrpLys 106  
 CC DB 268 AAATGTGCTGAGAAATCCAGGGGTGAACACTGTTCCCAAGATGCCAGATTTGGAAA 327  
 CC Qy 107 ProAspValLeuMetTyrrAsnSerAlaAspGluGlyPheAspGlyThrTyrGlnThrAsn 126  
 CC DB 328 CCGACATCTCTCTATAACGTGCTGATGCGCTGATGCGACATTCACATCAAC 387  
 CC Qy 127 ValValValArgSerGlyGlySerCsteuIrrValProProGlyIlePhelysSerThr 146  
 CC DB 388 GRTGTTGGTAATCTCTGGGATATGCGAGTACTGCTCCAGGCTATTCAAGSTTCC 447  
 CC Qy 147 CysLysMetAspIleAlaItpPhePropheAspAspGlnHisCysAspMetLysPheGly 166  
 CC DB 448 TGTTACATCGATGATGCTGCTGTTCCCTTGTGAGCATGCAACTGAGTTGGG 507  
 CC Qy 167 SerTrpThrTyrrAspGlyAsnGlnLeuAspLeuValIleLeuAspGluAlaGlyGlyAsp 186  
 CC DB 508 TCCTGCTCTACGGAGctTGCTGTCCTGATGCAATGAGCAGGAG-----GCAGAT 558



Db	328	CCGACATCTCTCTATAACAGTGTGCTATGGCTTGACCCACATTCACACTAAC	387	
Qy	127	ValValValArgSerGlyGlySerCysLeutLeuValProGlyIlePhalysSerthr	146	
Db	388	GTCCTGGTGAATTCTCTGGCATTTGCCATTCAGCTACCTGCCTCAGGCAATTAGTC	447	
Qy	147	CysLysMetAspIleAlaTrpPheProAspAspMetLysSerGly	166	
Db	448	TGCTACATCGGACTGCTGTTCCCTTGTGCAACTGAACTGAGTTGGG	507	
Qy	167	SerTrpTrpTrpAspGlyAsnGlnLeuAspLeuValLeuLysAspGluAlaGlyGlyAsp	186	RESULT 8 AYV12197
Db	508	TCTGGTCATGGGGTGGCTGATCGAGTCAGATGAGAG-----GCAGAT	558	AYV12197 standard; cDNA; 1876 BP.
Qy	187	IeuSerAspPheIleThrAsnGlyGlutTrpTrpLeuIleGlyMetProGlyLysLysAsn	206	XX
Db	559	ATCAGTGCTATATCCCCTAAATCGAGAATGGACCTACTGGGAATCTCCGGAAAGAGGAT	618	AC
Qy	207	ThrIleThrTrpAlaCysCysP-TGluProtTyrrValAspValThrPheThrIleMetIle	226	XX
Db	619	GAAAGGTTCTATGAGTGTGCAAAGGCCCTACCCCATGTACCTTOACATGACCATG	678	DE
Qy	227	ArgArgArgThrLeutTrpTrpPheAsnIleLeuValProCysValLeuIleSerSer	246	XX
Db	679	GCGCAGGACCTCTACTAGCCCTAAACCGCTGATCCCTGATCTCGCC	738	KW
Qy	247	MetAlaIleIeuLeuGlyPheThrIleProProAspSerClyGlyLysLeutLeuGlyVal	266	XX
Db	739	CTGCCTCTGCTGCTGCTCTCTACCTCTCATGCTGCTGAGATCATGCCGCAACA	858	FH
Qy	267	ThrIleLeuIleSerLeutTrpValPhlLeuAsnLeuValAlaGluThrLeuProGlnVal	286	FT
Db	799	ACAGTCCTTACCTCTCTACCTCTCATGCTGCTGAGATCATGCCGCAACA	958	FT
Qy	287	SerAspAlaIleProLeuLysLeuLysThrPheAsnCysIleMetPheMetValAlaSer	306	FT
Db	859	TCGAGTGGACCATGATGCCACTACTCGCCAGCACATGATCATCTGGGCTC	918	FT
Qy	307	SerValValLeuThrValAlaAsnTyrrHisIleGlyAsnGlyAsnGlyAsnGly	326	XX
Db	919	TGGGCTGCTGCTGCTGAGCGGTGATCGCGCAGAACCCGACGGGGCAAG	978	XX
Qy	327	MetProGlnIrrPheIleSerValPheLeuGlnInTripleProPrpIleLeuArgMetSer	346	XX
Db	979	ATGCCCAAGTGGACCAAGAGTACATCTCTGAACTGTTGCGTGTGAAATGAAAG	1038	XX
Qy	347	ArgProGlyLysLysIleThrArgLysThrIleMetMetArgGluIle	366	XX
Db	1039	AGGCCGGGAGGAGCACAGGGTGCCCGCCGCCAGACAGACAGCGCTGACGCTG	1098	XX
Qy	367	GlueLeuLysGluArgSerSerIleSerLeuIleAlaAsnValLeuAspIleAspAsp	386	XX
Db	1099	GCCAGTGTGGAGATGAGCCGGATGAGCCGGCTGGCG-----	1125	XX
Qy	387	PheArgHisGlyProProProAsnSerThrAlaSerThrGlyAsnLeu-----	403	CC
Db	1126	-----CGGCCGCC-----GCCAGCAACGGAACTCTGTACATC	1161	CC
Qy	404	-----GlyProGlyCys	407	CC
Db	1162	GGCTTCTGGCCCTGACGGGTGACTGTCCTCGACACTCTGGTAGTGTG	1221	CC
Qy	408	SerIlePheArgGlyAspPheArgGlySerPheValArgProSerThrMetGluAspVal	427	CC
Db	1222	GCG-----CCCATGGCCCTGCTCCCCACGGTACGATGAGCACCTC	1260	CC
Qy	428	-----GlyGlyGlyLeuGlySerHisArgGluLeuHisLeuIleLeuArgGluLeu	445	CC
Db	1261	CTGCAAGGGGGCAACCCCCCAGGGGACGGGACTTGGCAAATGAGGGTC	1320	CC
Qy	446	GlnPheIleIleAlaArgMetLysLysAlaAspGluGluLeuIleSerAspTyrP	465	CC
Db	1321	CGCTAATGGCAATGGCTCTGGCTCCAGAACGAGAACGGCAGTGG	1380	CC



XX	CC	A DNA sequence (AAT48239) codes for the alpha-7 subunit (AAW09025) of the human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp. mammalian cells or amphibian oocytes, carrying alpha-7 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids, (see also AAT48232-38, AAT48240-41), express recombinant nAChR subunits useful for identifying epis. that modulate the activity of human nAChRs
SQ	Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 U; 0 Other;	
Alignment Scores:		
Pred. No.:	2.02e-124	Length: 1876
Score:	1.258-50	Matches: 250
Percent Similarity:	63.23%	Conservative: 75
Best Local Similarity:	48.64%	Mismatches: 138
Query Match:	47.67%	Indels: 51
DB:	2	Gaps: 7
US-09-303-232-6 (1-501) x AAT48239 (1-1876)		
Qy	8 LeuAlaLeuAla--LeuLeuProValSerGluGlnGlyProHisGluLysArgLeu 26	
Db	100 CTGGCCTGGCTGCCGCGTCGCTCCTGCACGTGTCCTGAAAGCCAGTCCAGAGGAGTT 159	
Qy	27 LeuAlaAlaLeuAlaAsnTyraThrLeuGluArgProValAlaAsnGluSerIle 46	
Db	160 TACAGGACTCTAGAACTAACATCCCTGGTAGAACATCTGAACTGCTCCATTGCAA 219	
Qy	47 ProLeuGluValArgPheGlyLeuThrLeuGlnIleLeuAspValAspGluLysAsn 66	
Db	220 CCACTACCGCTCTACTCTCCTGAGCTCTGAGATCANGAGGATGAGAAAGAC 279	
Qy	67 GluLeuLeuIleThrAsnIleTerPheLeuSerLeuGluTrpAsnAspTyrAsnLeuArgTyrP 86	
Db	280 CAAGTTAACCAACATTTGGCTGCAAATGTCCTGGACAGATCATCTATTACAAGTGG 339	
Qy	87 AsnAspSerGluGlyTrpGlyValLysAspIleGluArgIleIleProAsnLysLeuTrpIlys 106	
Db	340 AATGNGTCAGAAATATCAGGGGTGAGACTGTTGCTGTTCCCGATGAGATTGZAAA 399	
Qy	107 ProAspValMetTyrAsnSerAlaAspGluGlyPheAspGlyIleThrGlnThrAsn 126	
Db	400 CCAGCATCTCTCTATAAGTGCTGATAGGCTGATAGGCACATTCACACTAAC 459	
Qy	127 ValValValArgSerGlyGlySerCysLeuItyrValProProGlyIlePheLysSerThr 146	
Db	460 GTGTGGTGAATTCTCTGGCCATTCAGTCCAGTACATTGAGATGTTCCAGTTC 519	
Qy	147 CysLysMetAspIleAlaIleTrpPheProAspAspGlnHisCysAspMetLysPheGly 166	
Db	520 TGCTCATCATGGCTGAGCTGTTCCCTTCATGTCAGCTGAACTGAGTTGGG 579	
Qy	167 SerTrpTrpIleAspGlyAsnGlnLeuAspLeuValLeuAspGluAlaGlyIleAsp 186	
Db	580 TCCGTGCTACGGGGTGTGCTCCGGATCAGAATGCGAGGAGG-----GGAGAT 630	
Qy	187 LeuSerAspPheIleIleTrpAsnGlyGluTrpTrpIleLeuIleGlyMetProGlyLysAsn 206	
Db	631 ATCATGGCTPATATCCCATGGAAATGGACATGGACCATGAGCTGACCTTCACAGTGACCATG 750	
Qy	207 ThrIleIleThrAlaCysCysProGluProTrpIleAspValIlePheThrIleMetIle 226	
Db	691 GAAAGCTCPATGAGCTGCTGAAAGAGCCCTACCCGATGTCAGTGGACATG 750	
Qy	227 ArgArgGlyThrLeuIleIleTrpPheAsnLeuIleLeuValLeuSerSer 246	
Db	751 CGCCAGGAGCTACTAAGGCTCAACTGCTGATCCCTGTCGATCAGTCGCGC 810	
Qy	247 MetAlaLeuIleGlyPheThrLeuProProAspSerGlyGluLysLeuThrLeuGlyVal 266	
Db	811 CTGGCCCTGCTGCTCCAGCTCTGAGATCCGGGAGAAGATTCCTGGGATA 870	
Qy	267 ThrIleLeuLeuSerIleThrValPheLeuAsnLeuValAlaGluThrLeuProGlnVal 286	

		RESULT	10
Db	871	ACAGTCTACTCTCTTACCGCTCTCATGCTGGCTGATCATGCCGAAACA	930
Cy	287	SerAspAlaLeuProLeuLeuGlyThrCysLysPheAsnCysIleMetPheMetValAlaSer	306
Db	931	TCCGATTGGTAACATTATAGCCCAAGTACTCCAGACCATTGATCATCGGCCTC	990
Cy	307	SerValYleLeuThrValValLeuAsnTyrThiSisArgThrAlaAlaAspIleHisGlu	326
Db	991	TCCGTGTCGGTGTGACGGTCAATCGRGCTGCAAGTACACACCACGACCCGAGGAAAG	1050
Cy	327	MetProGlnIrrPheIleLeuLeuGlnIrrPheIleLeuProIleMetArgMetSer	346
Db	1051	ATGCCCAAGTGACCGTCAATCGRGCTGCAAGTACACACCACGACCCGAGGAAAG	1110
Cy	347	ArgProGlyLysIleThrArgLysIleThrArgLysIleThrMetAsnThrArgMetArgGluLeu	366
Db	1111	AGGCCCGGGAGCACAGGGAACAGGGAACAGGCAAGGCCCTGGCTGGCTGTTGAATGTCGATGAAG	1170
Cy	367	GluLeuIysGluArgSerSerIleLeuLeuAlaAsnValLeuAspIleAspAspAsp	386
Db	1171	GCCAGTGTGGAGATGAGCCCTGGG	-----
Cy	387	PheArgHisGlyProIleProAsnSerIleSerIleLeuLeuAlaAsnValLeuAspIleAspAsp	403
Db	1198	-----CGCCGCC-----GCCAACCGGAACCTGCTGTAACATC	1233
Cy	404	-----GlyProGlyCys	407
Db	1234	GGCTTCGGGGCTGGCTGCACTGTGCCCCGACTCTGGGAGTAGTGTGT	1293
Cy	408	SerIlePheArgThrAppPheArgArgSerPheValLeuArgProSerThrMetGluAspVal	427
Db	1294	GCG-----CGATGGCTGCTCCCACGACGATGACCCCTC	1332
Cy	428	-----GlyGlyLysLeuGlySerHisIleArgGluLeuHisIleLeuArgGluLeu	445
Db	1333	CTGCAAGGGCAACCCCGAGGGGACTGGCCAGATCTGGAGGGGRC	1392
Cy	446	GlnPheIleThrAlaArgMetLysLysAlaAspGluGluAlaGluLeuLeuSerAspPTP	465
Db	1393	CGCTATAATGCCAATCCCTCGTGGCAGGAAACGAGCCTGCG	1452
Cy	466	LysPheAlaAlaMetValAlaAspArgPheCysLeuPheValPheThrLeuPheThrIle	485
Db	1453	AAGTTCGCCGCTGTGGTGAACCGCTGTCCTCATGGCCCTCTCGCTCACCATC	1512
Cy	486	IleAlaIleThrAlaValLeuLeuSerAlaProHisIleIle	499
Db	1513	ATCTGCACCAACGGCATCTGATGTCGGCTCCCAACTTCGTG	1554
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	ID	ABSS54875 standard; cdNA; 1876 BP.	
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	AC	ABSS54875;	
	XX		
	DT	06-DEC-2002 (first entry)	
	XX		
	DE	Human neuronal nicotinic acetylcholine receptor alpha 7 subunit cDNA.	
	XX		
	KW	Human; neuronal nicotinic acetylcholine receptor; nNACHR; gene; ss;	
	KW	ion flux; alpha 7 subunit.	
	XX		
	OS	Homo sapiens.	
	XX		
	FH	Key	Location/Qualifiers
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	FT	/tag= a	
	FT	/product= "Human nNACHR alpha 7 subunit"	
	XX		
	US6440681-B1.		





Db	1171	GCCAGTGTGGATGAGGCCGTGGCG	-----	1197
QY	387	PheArgHisGlyProProProAsnSerThrAlaSerThrGlyAsnLeu-----	-----	403
Db	1198	-----cccccGCCCC-----	-----GCACCAAACGGAACTCTGCTGACATC	1233
QY	404	-----	GlyProGlyCys 407	
Db	1234	GGCTTCCGGGCTGAGGGCTGCACTGTGTCCGACCCCGACTCTGGGTAGTGTT	1293	
QY	408	SerIlePheArgThrAspPheArgSerPheValArgProSerThrMetGluAspVal 427		
Db	1294	GGC-----	-----CGATGGCTGTCCCACAGCACATGGACACTC	1332
QY	428	-----GlyGlyGlyLeuGlySerHisArgGluLeuHisIeuIleLeuArgGluLeu 445		
Db	1333	CTGCA CGGGGAAACCCCCCGAGGGGACCCCGAACCTGGCCAAGAGATCCTGGAGGAGTC	1392	
QY	446	GlnPheIleThrAlaArgMetLysLysLysAlaAspGluGluAlaGluLeuIleSerAspDprP 465		
Db	1393	CGCTCATGCCCCATGCTGCTCCGTCGGAGGAGAAAGCGAGCCGGCTGCGAGCTGG 1452		
QY	466	LysPheAlaAlaMetValValAspArgPheCysLeuPheValPheThrLeuPheThrIle 485		
Db	1453	AAGTCGCGCCGCTGGTGGCCGGCTGCTGCTGCTCATGGCTTCATGGCTCITACACCAC	1512	
QY	486	IleAlaIleThrValAlaValLeuSerAlaProHisIleIle 49		
Db	1513	ATCTGACCATCGGCATCTGGATCTGGTGGCCGGCTCCAACTTCTGGT	1554	
RESULT 12				
ADA10864				
XX	ID	ADA10864 standard; DNA; 1876 BP.		
XX	XX			
XX	AC	ADA10864;		
XX	XX			
DT	06-NOV-2003	(first entry)		
XX	XX			
XX	DE	Human neuronal nicotinic acetylcholine receptor alpha 7 subunit DNA.		
XX	KW	ds gene; alpha 7 subunit; human; neuronal nicotinic acetylcholine receptor alpha 7 subunit DNA.		
XX	KW	synaptic transmission; gene therapy; transgenic.		
XX	KW	neuronal nicotinic acetylcholine receptor; ligand-gated ion channel;		
OS	Homo sapiens.			
XX	Key	Location/Qualifiers		
FH		1.		
FT	5'UTR	.72		
FT		/*tag= a		
CDS		73 . 1584		
FT		/*tag= b		
FT		/product= "nAChR alpha 7 subunit"		
3' UTR		1585 . 1876		
FT		/*tag= c		
XX	US6524789-B1.			
XX	25-FEB-2003.			
XX	07-JUN-1996;	96US-00660451.		
XX	07-JUN-1995;	95US-00484722.		
XX	(MERCK ) MERCK & CO INC.			
PA				
XX	Elliott KJ, Harpold MM;			
PI				
XX	WPI; 2003-511917/48.			
DR	P-PSDB; ADA10874.			
XX	New nucleic acid encoding an alpha-6 or a beta-3 subunit of a human neuronal nicotinic acetylcholine receptor (nAChR), useful for identifying compounds that modulate human neuronal nAChR activity.			
PT				
PT				
PT				







PT cell lines to conduct calcium ions, comprising specified concentrations  
 of ions of sodium, calcium and potassium at specified pH.  
 XX Claim 50; Page 69; 77pp; English.

CC The present sequence is the coding sequence for a mutant human alpha7  
 CC nicotinic acetylcholine Gated ion channel. The human alpha7 ion channel  
 CC was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3)  
 CC chimeric ligand-gated ion channel (see AAC90382 and AAB50014). The  
 CC alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells  
 CC in the present invention, resulting in preferential calcium ion  
 CC conductance by the cells. The protein encoded by this sequence has the  
 CC wild-type threonine residue at position 230 substituted by a proline  
 CC residue.

XX Sequence 1509 BP; 296 A; 452 C; 429 G; 332 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 6.42e-124 Length: 1509  
 Score: 1252.50 Matches: 249  
 Percent Similarity: 63.04% Conservative: 75  
 Best Local Similarity: 48.44% Mismatches: 139  
 Query Match: 47.44% Indels: 51  
 DB: 4 Gaps: 7

US-09-303-232-6 (1-501) × AAC90385 (1-1509)

QY 8 LeuAlaLeuAla--LeuLeuProValSerGluGlnGlyProHisGluLysArgLeu 26  
 DB 28 CTGGCGCTGGCGCGGCGGCGCTCGAGCTGAGTCAGTCAGGAGAACGCT 87

QY 27 LeuAsnAlaLeuAlaAsnTyrAsnThrLeuGluArgProValAlaAsnGluSerGlu 46  
 DB 88 TACAAGGAGCTGGTCAGAAACTACATCCCTTGAGAAGGCCGCAATGACTCGCA 147

QY 47 ProLeuIluValArgpheGlyLeuThrLeuGlnIleLeuAspPheGluLysAsn 66  
 DB 148 CCACTTCCCCTACTTCTCTGAGCTCAGCTCTGAGATCATGGACTGGATGAGAAC 207

QY 67 GluLeuIleThrAsnIleIleTrpIleSerGluIleTrpAsnAspTyrAsnLeuArgTrp 86  
 DB 208 CAAGTTAAACCACACATTGGCTGAAATGTCTGGAGAGATCACATTACATGG 267

QY 87 AsnAspSerGluItyrGlyIlyvalysAspLeuArgIleThrProAsnLysLeuTrpLys 106  
 DB 268 AATGTCCTAGATAATCGGGGTGAGGACTCTCGTTCCAGATGCCAGATGGAAA 327

QY 107 ProLeuIluMetTyrAsnSerAlaAspGluGlyPheAspGlyThrTyrGlnThrAsn 126  
 DB 328 CCAGACATTCCTCTCTATAACAGTGTGATGAGCGETTGAACGCTTACATCCACAAAC 387

QY 127 ValIluValArgpheGlyIlySerCysLeuIrrylProProGlyIleThrLeuIleSerThr 146  
 DB 388 GTGTTGTTGAAATCTCTGGCATTCAGTCCAGCTCAGGATATTAAAGTTGTC 447

QY 147 CysLysMetAspIleAlaTrpPheProPheAspAspGlnHisCysAspMetLysPheGly 166  
 DB 448 TGCTATACTGATGTTAAGTCGTTCCCTTATGTCAGATGCAAGTGGAGGG 507

QY 167 SerTrpThrTyrAspGlyAsnGlnLeuAspLeuValleuAspGluIaglyGlyAsp 186  
 DB 508 TCCTGCTCTTACGGGACCTGCTGAGATGGAACTGAGATCTGAGATTCAGGAT 558

QY 187 LeuSerAspPhenileThrAspGlyGluTrpIleGlyMetLysPheGlyLysAsn 206  
 DB 559 ATCAGTCGCTATATCCCCAATGGAGATGGACCTGAGATGGAACTCCGGCAAGAGGAGT 618

QY 207 ThrIleThrItyrTyrAlaCysProGluProTyroValAspValThrPheThrIleMetIle 226

DB 619 GAAAGTTCTTCTAGGTTCTGAAAGGCCCTACCCGATGTCACCTTCAGTGCACATG 678

QY 227 ArgArgArgThrLeuIrryTyrPhePheAsnLeuIleValProCysValLeuIleSerSer 246

Db 679 CGCCGAGGCCGCTACTATGGCTCAAACCTGGTGAATCCCCTGATGCTCATCTCGGCC 738  
 QY 247 MetAlaLeuIleUgLyPheThrLeuProProAspSerGlyGluIysLeuThrLeuGlyVal 266  
 Db 739 CTCACCCCTACTGGGTTCCCTCTGCTGAGATTCGGGATA 798

QY 267 ThrIleLeuLeuSerLeuIrrvalAlaGluThrLeuProGlnVal 286  
 Db 799 ACAGTCCTACTCTCTCTTACCTGGCTCATGGATCATCCCGAACAA 858

QY 287 SerAspAlaIleProLeuGlyIlyThrPheAsnCysIleMetPheMetValAlaSer 306  
 Db 859 TCCGATTCGGTACATTGATAGCCAGTAGTACTTCGCGACCATGATCACTGTCGCCTC 918

QY 307 SerValValleuThrValValLeuAsnTyryRishisArgThrAlaAspLeuHisGlu 326  
 Db 919 TCGTGTGGTGGGACGTGACTGACGACCCACGACCGACGGGCAAG 978

QY 327 MetProGlnIleTrpIleIlyserValAlaPheLeuGlnTrpLeuProTrpIleLeuArgMetSer 346  
 Db 979 ATGCCAAAGTGGCAAGTGGCCAGTCTGCTGAGCTGCTGTTGCTCTGAAATGAAAG 1038

QY 347 ArgProGlyLysIleThrArglysThrIleMetAsnThrArgMetArgGluLeu 366  
 Db 1039 AGGCCGGGAGGGAGAGGAGCAAGTGGCCCTGCGCAGCACAGAACGACGGGACTGCGACCTG 1098

QY 367 GluLeuIlyGluArgSerIleSerSerLeuLeuAlaAsnValleuAspIleAspAspAsp 386  
 Db 1099 GCAGTGTGGAGTGGAGTGGCGCTGGCG 1125

QY 387 PheArgHisGlyIlyProProProProProProAsnSerThrAlaSerThrGlyAsnLeu 403  
 Db 1126 ---CGCCGCC---CGCCGCC---CGCCGCC---CGCCGCC 1161

QY 404 ---GlyProGlyCys 407

Db 1162 GGCTTCGGCGGCCTGGACGGCGTGGACTGTGTCGGACGCCCCGACTCTGGTAGTGTGT 1221

QY 408 SerIlePheArgThrAspPheArgArgSerIleAspSerIleAspIleAsp 427  
 Db 1222 GGC---CGCATGGCCCTGCTCCCCACGACGATGAGGACCTC 1260

QY 428 ---GlyGlyGlyLeuGlySerRishisArgGluLeuHisIleLeuArgGluLeu 445  
 Db 1261 CTGAGGGCGCAACCCCCGAGGGGACCCGGACTGGCCAAGATCCGGAGGGTC 1320

QY 446 GlnPheIleThrAlaArgMetLysLysAlaAspGluGluAlaGluLeuIleSerAspTrp 465  
 Db 1321 CGCTACATGGCAATGCTGCTCCCGCAGGAAAGCGAGGCGGCTCTGAGGATGTTGG 1380

QY 466 LysPheAlaAlaMetIleValValAspArgPheCysLeuPheValPheThrLeuPheThrIle 485  
 Db 1381 AAGTTCGGCCCTCTGGGAGCCGCTCATGGCTCATGGCTTCACCATC 1440

QY 486 IleAlaIleThrValAlaLeuLeuSerAlaProHisIle 499  
 Db 1441 ATCTGACCATGCGATCTGGCTCTGATGCGTCCACATTCTGTC 1482

Search completed: May 8, 2004, 19:30:45  
 Job time : 554.234 secs



Qy	12 ALLPVSEQQBHEKRLLNALLANYNTLERPVANESEPLEVERFGLTQQIDVDEKNQLLIT 15 SLLHVSLOGDFQRKLYKELVNLNFPLRFLYANDSPLTVFPLSLLQIINVDENQVLIT	71	Qy	67 QLLITNIWLSLEWNDYLNRLNDSEYGGVKDILRITPNKLWKPDVLMNSADEGFDGTYQTN 70 QVLTNTNWLMSWTHYLQNMSETPGVNRPFGQINPKDILYNSADERFDATEHTN	126
Db			Db		
Qy	72 NIWLSLEWNDYLNRLNDSEYGGVKDILRITPNKLWKPDVLMNSADEGFDGTQTYQTNVYRS 75 NIWLNQSWTHYLQNMSETPGVNRPFGQINPKDILYNSADERFDATEHTN	131	Qy	127 VVRSGGSCLYXVPGLFKSTCKMDIAWFPEPDQCDMKERGSWTYDGNOQLDVLKDAGGD 130 VLVAISGHCOYLPGLFKSCYIDRWFQDVGKLRGSWSWGWSLDLQME--AD	186
Db			Db		
Qy	132 GGSCLYXVPGLFKSTCKMDIAWFPEPDQCDMKFQSSWTDGNQDLVLKREAGDLSDFI 135 SGHCQYLPGLFKSCYIDRWFQDVGKLRGSWSWGWSLDLQME--ADISGYI	191	Qy	187 LSDFTINGWYLGMPKGKONTITYACCPEBYDVTETIMTRRRLYYFNLIVPCVLISS 188 ISSYPNGENDLMLGPGRNEKFBCCKEYDPDTYTTVMRRRLYYGMLNLLIPCVLISA	246
Db			Db		
Qy	192 TNGEWLIGMPGKNTITYACCEPVDVIFTIMTRRRLYYFNLIVPCVLISSMALLG 192 PNGEWLIGPGKSERFYCCKEYDPDTFTVMBRRTYYGMLNLLIPCVLISALLY	251	Qy	247 MALLGETLPDDPSGEKLTGWTILSLTFNLVATELPQVSDATAFLGLYFNCFMFIVAS 248 LALAYELLPADSGEKSLSLGTIVLSSLTFNLVATELPQVSDATAFLGLYFNCFMFIVAS	306
Db			Db		
Qy	252 FTLPPDSGEKLTGWTILSLTFNLVATELPQVSDAIPLLGTYFNCTMFIVASSVILIT 252 FLLPADSGEKTSGLTGWTILSLTFNLVATEIMPATSDSVLIAQYFASIMLIVGLSVVIT	311	Qy	307 SVVLTIVVUNYHHRTAIDIHMMPQWIKTSVFLQWLPMILRMSPRGKLTTRKTMNTRMREL 307 SVVVTIVLRYHHDPDGKMPKWRTRILLNWCAFLRMKRPGEDKVPAQCQHKPRRCSL	366
Db			Db		
Qy	312 YVVIJNYHRTADITHMPQWIKTSVFLQWLPMILRMSPRGKLTTRKTMNTRMREL 312 VIVLOYHHDGGKMPKWRTRILLNWCAFLRMKRPGEDKVPAQCQHKCORCSLASVEM	371	Qy	367 ELKERS---KSSLANVLDIDDDFR---HGPPPNSTASTGNLGPQCS1FRTDFFRS 367 ASVIEASAGGAPPTSGNLVLYI-GFRGLESMHCAFPDGSVVCGLI-ACSPPTDDEHLMH	422
Db			Db		
Qy	372 SSKSLANVLDIDDDFRHGPAPPNSTASTGNL---GPGCISIERT 372 SAV---ASNGNLTYGFGVHCVPTPDSGVYVG---	412	Qy	418 FVRPSTMEDVGGGLGSHFHRLHLLRELQFTTARMKKADEEAEILSDWKPAAMTYDRFCL 423 GTHPSDGDF-----DLAKTLEEVRTANRERCODESEVICSEWEKAACVYDRLCL	477
Db			Db		
Qy	413 DFRRSVPRTSMEDV -GGGGSHSHREHLTLRELQFTTARMKKADEEAEILSDWKFAAM 409 --RMACSPTHDEHLHGGQPPEGDPLAKTLEEVRYIANRERCQDESEAVCSEWKFAAC	470	Qy	478 FVFTEFTIATVAVLSSAPHII 499 473 MAFSVTTIICHTIGILMSAPNFV 494	499
Db			Db		
Qy	471 VVDRFCLEFVFTLTIATVAVLSSAPHII 499 466 VVDRCLMAFSVFTICTIGILMSAPNFV 494	499	RESULT 3 JN0113	nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken N;Alternate names: alpha-bungarotoxin-binding protein alpha chain C;Species: Gallus gallus (chicken) C;Date: 12-Feb-1993 #sequence revision 12-Feb-1993 #text_change 20-Aug-1999 C;Accession: JN0113; JH0172; S26566 R;Courtourit, S.; Bertrand, D.; Mitter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N.; Neuron 5, 847-856, 1990 A;Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmental A;Reference number: JN0113; MUID:91097796; PMID:1702646 A;Accession: JN0113 A;Molecule type: DNA A;Residues: 1-502 <COU> A;Cross-references: GB:X68586; NID:9287756; PID:CAA48576-1; PMID:g287757 A;Experimental source: white leghorn; brain R;Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J. Neuron 5, 35-48, 1990 A;Title: Brain alpha-bungarotoxin binding protein cDNAs and mAbs reveal subtypes of thi A;Reference number: JH0172; MUID:90315158; PMID:2369519 A;Cross-references: EMBL:X52295; NID:963077; PIDN:CAA6543-1; PMID:963078 A;Experimental source: brain R;Mitter,Sadzinski, L.; Hernandez, M.C.; Roztocil, T.; Ballivet, M.; Matter, J.M. EMBO J. 11, 4529-4538, 1992 A;Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor promoter d A;Reference number: S28018; PMID:93049204; PMID:1425587 A;Accession: S28018 A;Molecule type: DNA A;Residues: 1-18 <MBS> A;Cross-references: EMBL:X68246; GB:S49751; NID:965319; PID:CAA48317-1; PMID:g65320 A;Experimental source: white leghorn; erythrocyte R;Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.; R Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985 A;Title: Brain and muscle nicotinic acetylcholine receptors are different but homologou A;Reference number: A94055; MUID:85270494; PMID:3860855 A;Accession: B25738 A;Molecule type: protein	499
Db			Db		

RESULT 2  
A57175

nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse

C;Species: Mus musculus (house mouse)

C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 20-Aug-1999

C;Accession: A57175

R;Orr-Urtreger, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L.

Genomics 26, 389-402, 1995

A;Title: Cloning and mapping of the mouse alpha7 neuronal nicotinic acetylcholine receptor

A;Reference number: A57175; MUID:95324936; PMID:7601470

A;Accession: A57175

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-502 &lt;ORR&gt;

B;Cross-references: GB:137663; NID:9790853; PIDN: AAC42053-1; PMID:g790854

C;Superfamily: acetylcholine receptor

C;Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein;

F:1-23/Domain: signal sequence #status predicted &lt;SIG&gt;

F:24-502/Domain: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted &lt;TR1&gt;

F:231-254/Domain: transmembrane#status predicted &lt;TR1&gt;

F:262-280/Domain: transmembrane#status predicted &lt;TR2&gt;

F:296-317/Domain: transmembrane#status predicted &lt;TR3&gt;

F:470-488/Domain: transmembrane#status predicted &lt;TR4&gt;

F:46-90,123/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:365-413,427/Binding site: phosphate (Ser) (covalent) #status predicted

F:415/Binding site: phosphate (Thr) (covalent) #status predicted

F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match Score 47.6%; Length 502;

Best Local Similarity 49.6%; Pred. No. 7e-99;

Matches 249; Conservative 78; Mismatches 148; Gaps 27; Gaps 7;

Oy 8 LALAAALHVSLQEFQRLYKELVNNYNPLERPVANDSQFLTVYFSLSLQIMDYDEK 66

Oy 10 LALAAALHVSLQEFQRLYKELVNNYNPLERPVANDSQFLTVYFSLSLQIMDYDEK 69

Db

A;Residues: 24-25,'ET',28-41,'X','43-45,'X','47 <CON>  
 C;Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized  
 A;Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 330/3  
 C;Superfamily: acetylcholine receptor  
 C;Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein;  
 F;1-23/Domain: signal sequence #status predicted <STR>  
 F;24-50/Domain: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted  
 F;21-23/Domain: transmembrane #status predicted <TR2>  
 F;166-210/Domain: transmembrane #status predicted <TR2>  
 F;196-317/Domain: transmembrane #status predicted <TR3>  
 F;4/48/Domain: transmembrane #status predicted <TR4>  
 F;16, 90, 113/Binding site: carboxylate (Asx) (covalent) #status predicted  
 F;145, 367, 413, 427, 465/Binding site: phosphate (Ser) (covalent) #status predicted  
 F;415/Binding site: phosphate (Thr) (covalent) #status predicted  
 F;442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 47.4%; Score 1252.5; DB 2; Length 502;  
 Best Local Similarity 4.8%; Pred. No. 1..3e-98;  
 Matches 249; Conservative 74; Mismatches 140; Indels 51; Gaps 7;

Qy 8 LAL-LIPVSEOGPHEKRLLNLLANTLTERPVANESEPLEVRFGTLTQQIDVDEKN 66  
 Db 10 LALAAAHVLSQEEFQRKLYKELVKNYPLERPVANDSQPLTVYFSNLQLQIMDVEKN 69

Qy 67 QLITINIVSLEWNDYLNRLWNSSEYYGGYKDLRITPNKLWKPDMYNSADEGFDGTQTN 126  
 Db 70 QVLTTNIVQMSWTDHYLQWNNSSEYPGVTKVREPDGQIWKPDILYNSADERDATFTN 129

Qy 127 VVYRSGGSCLYVPPGIEFKSTCKMDIAWFPDDOHCMDMKGSMTYDGNQDLVLKDEAGGD 186  
 Db 130 VLYNPSGICQYLPPIGFKSSCYDVRWMPEDVYHCKLGKFGSWYGYGWLDLQNQE--AD 186

Qy 187 LSDEFITNGEWYLIGMPGKNTITYACCEPYDVTFTMIRRTLYFNCIMFWVAS 246  
 Db 187 ISGYIPNGSEMDLVGPGKRSERYVECCKEKPDPYDFTVMMRRTLYGUNLIPCVLISA 246

Qy 247 MALIGFTLPDGSERKLTGVTLLSLTVFLNLYAETLPQVSDAIPLLGTYFNCIMFWAS 306  
 Db 247 LALLVFLPADSGEKISIGITVLLSITVFLLYAIMPATSDSYVLTQYFASTMIIVGL 306

Qy 307 SYVLTWVLYNHRTADTHEMPWIKSVFLOWLWLMRSPGKTKTMMNTMRREL 366  
 Db 307 SVWVTVILQYHHHDPDGSKRMPKWTRVLLNWAWFLRMKRPGEKDVKPACQHKQRSSL 366

Qy 367 ELKERSKSLLANVLDIDDDFRHGPVPNASTGNL-----  
 Db 367 ASYEMSAV-----  
 Qy 408 SIFRTDFRSFVFPSSTMVDV--GGGLGSHHREJHLIRELQFTARMKKADEAEALISDW 465  
 Db 408 G----RMACSPTHDEHLLHGQQPGDPDLAKLKEEVRYIANRFRQCDSEAVCSEW 460

Qy 466 KFAAMWVDRFCLEFLFTIATVAVLILSAPHTI 499  
 Db 461 KFAACVVDRCLIMAFAVSFTLICIGILMSAPNFV 494

RESULT 5  
 Db T01378 nicotinic receptor alpha 7 chain - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: T01378  
 R;SequeLA, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.  
 A;Title: Molecular cloning, functional properties, and distribution of rat brain alpha  
 A;Reference number: Z14310; PMID:93147931; PMID:6778857  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-502 <SEG>  
 A;Cross-references: EMBL:S33987; NID:9264770; PIDN:AAB25224-2; PID:95705903  
 C;Superfamily: acetylcholine receptor

Query Match 47.2%; Score 1246.5; DB 2; Length 502;  
 Best Local Similarity 4.9%; Pred. No. 4..1e-98;  
 Matches 248; Conservative 78; Mismatches 149; Indels 27; Gaps 7;

Qy 8 LAL-LIPVSEOGPHEKRLLNLLANTLTERPVANESEPLEVRFGTLTQQIDVDEKN 66  
 Db 10 LALAAAHVLSQEEFQRKLYKELVKNYPLERPVANDSQPLTVYFSNLQLQIMDVEKN 69

Qy 67 QLITINIVSLEWNDYLNRLWNSSEYYGGYKDLRITPNKLWKPDMYNSADEGFDGTQTN 126  
 Db 70 QVLTTNIVQMSWTDHYLQWNNSSEYPGVTKVREPDGQIWKPDILYNSADERDATFTN 129

Qy 127 VVYRSGGSCLYVPPGIEFKSTCKMDIAWFPDDOHCMDMKGSMTYDGNQDLVLKDEAGGD 186

Db	13.0	VLYNAGSHCQYLPPGJFKSSCYIDVRWFEPDVQQCKLKPEFWSWYGGWSLILQMQE--AD	186	300	MIVVTTASTVFITYVNLHYRPETHDMGPWTNLLYWIPWLRLRPGHNLTYASLPSL	359		
Qy	187	LSDFITNGEWYLIGMPGKNTTITYACCPBPYVDFTFTIMRRRTLYFFPNLIVPCVLSS	246	359	MNTRMRELELKERSSSKLANYLD-----IDDFRHGPPPNNSTASTGNLGPBCS	408		
Db	187	ISSYVPPNGEDVLMGPGKRBKFYCRKEYPPDVTYTVMRRRTLYYGLNLIPCVLSS	246	360	FSTK-----ENRHSSLIRATKDNDNSHLSSANSEFDACRNQYINTQSVSNGLTLG-S	412		
Qy	247	MALGFTLPDSGEKLTGTYTLLSLTVFLNVAETLPQYSDAIPLLGYFNCFIMFVAS	306	409	I FRTDPRRSFVRPSTMEDVGAGLGSFHRE---LHLILREQLQFITARMKKADEAEELIS	463		
Db	247	LALLYFLPDSGEKLSGTLVLLSLTVFLNVAIMPASDVSPLIAQFASTMTIVGL	306	413	1-----PTMISSNGNTTDSQATLILRUYHEKIVKRMIECDKEEQACN	461		
Qy	307	SVLTIVVYHNVHHRDIADHMPQWIKSVFQWLPIIILMRSPGRCTRKTMANTMRML	366	464	DWKFAAMMVVDIFCLFYTFHTLFTIATAVLLSAPHI	499		
Db	307	SVVYVIVLRYHHHDPDGGMCPKWTRILLNWCMFLMRKGDKVKRPCQHQKPRCSL	366	462	NWKFAAMMVVDLCLIVYFTIPIVSTGIFWSSAPYLV	497		
Qy	367	ELKERSS---KSLLIANVLDIDDDFR----HGPPPPNSTASTGNLGPCCSIFRDFRS	417	RESULT 7				
Db	367	ASVLSAGACPPTSNGNLII-GRFGLBEMHCAPTPDSSEVCVGL--ASCPTHBEHLM	422	alphabungarotoxin-binding protein alpha-2 chain precursor - chicken				
Qy	418	FVRPSTMEDVGGLGSHHRELHLIRELQPITARMKKADEAEELISDWRFCU	477	C;Species: Gallus gallus (chicken)				
Db	423	GAHPSDGDP-----DLAKLCLEEVRYTIANNRQDSEVICSEWEKAACVYDPLCI	472	C;Accession: JH0173				
Qy	478	FVFLFIFTIATVLLSAPHI	499	R;Schoepf, R.; Corroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.				
Db	473	MAFSVFTIICITGILMSAPNFV	494	Neuron 5, 35-48, 1990				
A;Title: Brain alpha-bungarotoxin binding protein cDNAs and Mabs reveal subtypes								
A;Reference number: JH0172; MUID:90315158; PMID:2269519								
A;Accession: JH0173								
A;Molecule type: mRNA								
A;Residues: 1-511-<SCH>								
A;Cross-references: GB: X52296; NID: 963001; PIDN: CAA36544; PMID: 9630082								
A;Experimental source: brain								
A;Note: this sequence is similar to acetylcholine receptor alpha chains								
C;Comment: Alpha-bungarotoxin binding proteins are localized to extrasynaptic pre-								
C;Keywords: acetylcholine receptor								
C;KeyWords: Glycoprotein, transmembrane protein								
F;1-30/Domain: signal sequence #status predicted <SIG>								
F;31-510/Domain: alpha-bungarotoxin binding protein alpha-2 chain #status predicted <SIG>								
F;239-262/Domain: transmembrane #status predicted <TM1>								
F;270-288/Domain: transmembrane #status predicted <TM2>								
F;304-323/Domain: transmembrane #status predicted <TM3>								
F;479-496/Domain: transmembrane #status predicted <TM4>								
F;54/Binding site: carbohydrate (Asn) (covalent) #status predicted								
Query Match								
Score 46.5%; Best Local Similarity 46.5%; Pred. No. 2.1e-56;								
Matches 246; Conservative 75; Mismatches 134; Indels 73; Gaps 9;								
Qy								
5 LAALAILLALLIPVSEQGPHEKRLLNALLANTNLERVANEPEPLERFGLTQQIDDVDE								
16 IWASLLESPFKVSSQOESQRRLYDILRNINRLERVMNDSQPIVTELOLSLQI1DVDE								
17 KNOQLTNTNLSLENDNDYLRWNDSYGGYKVDLRTPKNLUKWPDKVMDYNSADEGFTYQ								
18 KNOQLTNTNLSLENDNDYLRWNDSYGGYKVDLRTPKNLUKWPDKVMDYNSADEGFTYQ								
19 GDLSDITINGWYLLGMPGRKNTTITYACCPBPYVDFTIMIRRPLYYFFNLIVCVL								
20 185 GDLSDITINGWYLLGMPGRKNTTITYACCPBPYVDFTIMIRRPLYYFFNLIVCVL								
21 193 ADISNYXISNGEWDLVVGVPGRNNEYECCKEPYPDVDTYTITMRRRLTUYGUNLILFCVLI								
22 194 245 SSMALJGFTLPPDSGEKRLTGVTULLSLTFLVNLVATYLPOVSDAPLUGTYFNCIMEMY								
23 253 SGLLAVFLPAPDSGEKRLTGVTULLSLTFLVNLVATYLPOVSDAPLUGTYFNCIMEMY								
24 254 ASSVYVLTUVVLYHNRTAIDHEMPWIKSYFLQMLWFLRMSRPGKXTRKTMNTRMR								
25 255 ATGFDISEITNGEWALPPTVERNEKYDCCBEPYDHFYHMRRLTYYGFNLIMP								
26 256 CVALSSMALIGFTLPPDSGEKRLTGVTULLSLTFLVNLVATYLPOVSDAPLUGTYFNCIMEMY								
27 257 GLSVYVTVLVLQFHHDPOAGKMPWRVILWNLCAWFRLMKKPGNIN-----K								
28 258 CILATLMTMGTLLPDAKGKTTQITVNLSCFLSISMSPTSEAVPLGIFTFC								
29 259 QY ERSSISLLANVLDIDDDFRHGPBPPNSTASTGNLGPBCS								
30 260 365 ELELK-----ERSSISLLANVLDIDDDFRHGPBPPNSTASTGNLGPBCS								
31 261 366 FGPGSIF 410								
32 262 367 FGPGSIF 410								
33 263 368 FGPGSIF 410								
34 264 369 FGPGSIF 410								
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111 341 446 FGPGSIF 410								
112 342 447 FGPGSIF 410								
113 343 448 FGPGSIF 410								

Db	362	PLSCKSYFPKHHPSLQNTENMVL-----PGHQPSNGNNMTIYHTMENPCC--	406	RESULT 9
Qy	411	RITDFFRSRTPRSFMDVGGIG-----SHREHHL-----ILRBLQFTAR	451	Tl9862
Db	407	-----PQN-NDLGSKSGKRTCTPLSEDNEVQVKALMDTIPVTKILEVQF-TAMR	455	hypothetical protein C40C9.2 - Caenorhabditis elegans
C;Species:				
C;Date:	15-Oct-1999	#sequence_revision 15-Oct-1999	#text_change 18-Feb-2000	
C;Accession:	Tl9862			
R;Embry.	C.			
Db	452	MKGADEEAFLISDWRKFAAMVDRFCLFVTFLTFTIATAVLLSAPHII	499	submitted to the EMBL Data Library, March 1996
A;Reference number:	219188			
A;Accession:	Tl9862			
A;Status:	preliminary; translated from GB/EMBL/DDJB			
A;Molecule type: DNA				
A;Residues: 1-542 <WIL>				
A;Cross-references: EMBL:U88167; PIDN:AAB4223.1; GSDB:GN00019; CESP:D2092.3				
A;Description: The sequence of C. elegans cosmid D2092.				
A;Accession: T25671				
A;Status: preliminary; translated from GB/EMBL/DDBJ				
A;Molecule type: DNA				
A;Residues: 1-461 <GAT>				
A;Cross-references: EMBL:U88167; PIDN:AAB4223.1; GSDB:GN00019; CESP:C40C9.2				
A;Description: The sequence of C. elegans cosmid D2092.				
A;Accession: T25671				
A;Status: preliminary; translated from GB/EMBL/DDBJ				
A;Molecule type: DNA				
A;Residues: 1-461 <GAT>				
A;Cross-references: EMBL:U88167; PIDN:AAB4223.1; GSDB:GN00019; CESP:C40C9.2				
A;Description: The sequence of C. elegans cosmid D2092.				
Query Match	42.9%	Score 1132; DB 2; Length 461;		
Best Local Similarity	44.7%	Pred. No. 2. Le-88;		
Matches 216; Conservative 86; Mismatches 127				
C;Superfamily: acetylcholine receptor				
Query	23	EKRULNALLANTTLERPVANESEPLEYRFGTLQQITIDVEKNQLITNIWLSLENNY	82	Qy
Db	26	ETKIFTDLKGYNPERPQNSQLEPKTKLFLQIILVDEKNQIIVSNASVYTWDH	85	10 LIAlIPVSQGPHEKPRBLNALLANTTLERPVANESEPLEYRFGTLQQITIDVEKNQLI
Qy	83	NLRNDNSEYGGVKDLRI-TPNKLWKPDVLMNSADEGFDGTQTNVYVRSGGSLVYPP	140	11 LFIHLLTEVSSADEYRLIADLRHNYDPYERPVANASEPLUVSVTKYLQQLDVEKNQVYI
Db	86	KLQWEPKKKGGIQQDTRPSSSDHTWKPDVLYNSAAEDDSTFKSNLITVHTGTVVNTPP	145	12 ITINWLSLEWDNYLNRLWNSDEYGVKDRLRI-TPNKLWKPDVLMNSADEGFDGTQTNVY
Qy	141	GIFKSTCKDIAWPFDDECDMKMFGSWTYDGNQDILVKEDEAGG---DLSDPITNGEW	196	13 7LYWNLIEQWTDYKLUKDWPSEYGSIKTRIPGNANA1MKPDVLYNSADENPDSTYPTVY
Db	146	GVLKFKVQOLDVTWPFDDQVCEMFAGWSWFFHGVAIDQIDDINGTQSMDLSTYLVNGW	205	14 10 LIAlIPVSQGPHEKPRBLNALLANTTLERPVANESEPLEYRFGTLQQITIDVEKNQLI
Qy	197	YLIGMPGRKNTIYACCPEPYDVDTFTIMIRRLLYFFNLIYPCVLISSMALLGFTLPP	256	15 17 IGLRQQTDFEYFYQOHNLMPVAPBEMTPRVTSKOMAESYEDVMTLNKYMOKA
Db	206	QVISTNAKRVSYKCPDPYPTVNLVIRRLYFGNLIFSLLSLMAGFMPP	265	16 41.2
Qy	257	DSGRKLTQTVTILLSLTVNLVAAETLPQYSDAIPLGTYCNYCIMEMYASSVYLVVNL	316	17 KTMIMNTMRMELLEKRSKSSLANVLDLDDDFRHPPPPNSTASTGNLGP-GCSIRT
Db	266	DAGERKLTLETVLILAVFPLSMVSEMTPTSEAVPLGFESCCNLVVAASVYFTIVLN	325	18 41.3
Qy	317	YHRTADIMEMPQWIKPSVYLOWLWILNSRPGKXITRKTTIMNTRMRELLEKRSKSSL	376	19 41.7
Db	3226	LHFSAADSHEMNPLVRVLEFLPWLLNSRPGKXFRVK-----	-	20 43.9
Qy	377	LANVLDIDDFRHGCPPNPNSTASTGNLGCGCSIRTDFFRSFVRPSTMEDVGGGLGSRR	436	21 43.9
Db	364	-ANVIDSTDKMPKKPKNPLD-----CNL-----PSN---HAGYEQIL	397	22 44.7
Qy	437	ELHLLIRELQFITARMKKADEAEELISDWFKAAMYVDRFCFLFVFTLTITAVVLLSAP	496	23 44.7
Db	398	LLHSVHTELRVVAFYNEKHEDEQDQTDWFAAMVDRCLLFTVTVISILAIMMSAP	457	24 45.6
RESULT 10				
Qy	497	HII 499		Tl9622
Db	458	HII 460		hypothetical protein C31H5.3 - Caenorhabditis elegans
C;Species:				
C;Date:	15-Oct-1999	#sequence_revision 15-Oct-1999	#text_change 21-Jan-2000	
C;Accession:	Tl9622			

R. Kerishaw, J.	A. Submitted to the EMBL Data Library, April 1997
A. Reference number: Z19153	
A. Accession: T119622	
A. Status: preliminary; translated from GB/EMBL/DDBJ	
A. Molecule type: DNA	
A. Residues: 1-560 <WIL>	
A. Cross-references: EMBL:Z93778; PIDN:CAB07843.1; GSPDB:GN00019; CESP:C31HS.3	
A. Experimental source: clone C31HS	
C. Genetics:	
A. Map Position: 1	
A. Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3	
C. Superfamily: acetylcholine receptor	
Query Match Score 40.9%; Score 1081; DB 2; Length 560; Best Local Similarity 39.4%; Pred. No. 6e-84; N mismatches 88; Matches 218; Conservative 88; Indels 92; Gaps 8;	
20 GPHEKRLLNALLANTNTLERPVANESEPLEVRERGLTLOQITDVDEKNQLLTINIMLSLEW 79 28 GDHERRLYAKLAENNNKLARPVRNESEAVVLLGMDYQQIDIDEKHQIMNSNVWRMSW 87	
80 NDYNURWNDSSEGGYKDLRTPNKLUKPDKVLMYNSADEFGDGTQTNWVWSGGCLIVV 139 88 TDHYLTWDPEFGNKEKVLUPPINNIWKPDVLYNSYDQOPETSWPNAVVLTYGNTWIP 147	
140 PGIFKSTCMNDIAWPPDDHDCKMKEGSWYDGQNQDVLKMDEAGGDLSDTINGEWYL 199 148 PAIIRSSCAADIAVAPPEDQHCTMKGWSWYSGFPTDLI --NTTISPAITYKPNSEWELL 204	
200 GMPCRKNTITYACCEPEPYDVTFTIMIRRRTLYTFENLTVCPVLISSMALIGFTLPPDSG 259 205 GLTQSRSIFFYCCCEPYDVTFTFSIRRLTYGENLICPCMFLSSALSFTPADCG 264	
260 EKLIGTGTLLSLTFLNLTVAETLPLQVSADPLIPLGTYFCMTMFYMASSVLTUTDVLNHH 319 265 EKLNLGVITFMSLCYFMIAEAMQTSDALPLIQTYSCLMFQGASVTTAVIALNFHH 324	
320 RTADLTHE-MPQWIKSVFLOWLPWLWIRMSRP-----GRKITHTRIMNTRMR 364 325 RSPQYKPNKPKLTKLIGMPTLGMERDVYLESVKAGYIASDNKKQRQYILLEVERH 384	
365 ELELKERSSSKLLANVLDD-----DDFRHGPPPNSTAST--GNLGPCCSIRTDFFR 415 385 ILTRPNGNHSAYDVKAVHDLSTGNPHSDAKSSPSPKRTSASINGMTG ----- 433	
416 RSPYTPSPSMEDGGGICS----- 433 434 ---LPTT---QMNGALDSSINKYCTKVTRPLENGSATINHKSSPQINPNNNNYKCAN 487	
434 ---HEBELHLTLRELOFTARMKKADEAEELISDWKEAAMYVDRCLFLVFVFTLFTIIA 487 488 NKQTKQFEDRHFHHLNEVRVISARVRKEKAMHALQADMFASRVVDRCFLAFSAFLFMC 547	
489 TAVVLLSAPHIIV 500 548 TAIISSYNAPHLFV 560	
A. Residues: 30-503 <ANA>	
A. Cross-references: EMBL:X53559; PIDN:CAA37625.1; PID:q34986	
C. Genetics:	
A. Gene: GDB:CHRNA3	
A. Cross-references: GDB:125219; OMIM:118503	
A. Map position: 15q24-15q24	
C. Superfamily: acetylcholine receptor	
C. Keywords: neurotransmitter receptor	
Query Match Score 37.5%; Score 989; DB 2; Length 503; Best Local Similarity 38.9%; Pred. No. 3 e6-76; N mismatches 202; Conservative 91; Indels 62; Gaps 6;	
1 MAPMLAAALLALLPVSEQGPHEKRLLNALLANTNTLERPVANESEPLEVRERGLTLOQII 60 Db 12 VAURL-LUMLLSSLPVALASEAHRFLFERLFEDYNEIIRTPVANYSDPVTHFEVMSQLV 70	
Qy 61 DYDEKIQQLITINIWLSLEWNDYLRLWNDSSEGGYKDLRTPNKLUKPDKVLMYNSADEGFD 120 Db 71 KVEDVNQIMETNWNLWKLQIWNWDYKLKWNSDYGGAEMRYYPAQKWKPDIVLYNNAVGDFQ 130	
Qy 121 GRYQTQNVYVRSQGGSCLYVPPGIFKPKSTCRMDIAWPFEDDHCMDMKFGSWYTDGNQDVLVX 180 Db 131 VDDKTALKKYTGTEVWTPPAIFKSSCKIDVITYFPFDYDNCMTKFGWSWSDKAKLDVLII 190	
Qy 181 DEAGGDLSDFITNGEWLJGMGPKKNITITYACCEPEPYDVTFTIMIRRRTLYYFNLIVP 240 Db 191 G-SMMNKKDYWESGEWAIKAPSYKHDIKYNCCEBIPDTISLYRRLPLFYTNLIIIP 249	
Qy 241 CULISSNALLGFTLPPDGSQEKTGLGTVILLSLTVFLNLYVAETLPQVSADAPIPLGTYFNCL 300 Db 250 CLISLSELTVLPYLPSPDCEGKVTLCISVSLSLTVFLVLTETPSTSVMPLIGEYLLFT 309	
Qy 301 MFMVASVVLTVYVNLNTHTRADHEPMQWIKSVFLOWLPWLWIRMSRPKKITRKTIMMN 360 Db 310 MFTVTLISIVTYVFLNHYRTPHTHMSWVKTIVFLNLPRVFMTRP----- 357	
Qy 361 TRMRELLKEKRSKSLLANVLDDDFRHGPPPNNSTASTGNL-----GPGCS----- 408 Db 358 -----TSNEGNAQKPKRPLGAGELSNLNCFRSAESKGCKEGYPC 395	
Qy 409 -----IERTDFRSPYRPTSMEDVGG - GLGSHHREHLILRELOQFTTARMCK 454 Db 396 QDGMCGYCHHRRKIKNSFANSANLRTSSSESSVDAVLSALSPEIKEAIDOSVSKYTAENMKA 455	
Qy 455 ADEEEAELISDMKPAAMVYDRCFLFVFVFTLFTIIATVAVL 493 Db 456 QNEAKEIQQDWKVKYAMVMDRFLWFLVCLTAGLFL 494	
RESULT 12	
A. Residues: 1-503 <WIL>	
A. Cross-references: EMBL:Z93778; PIDN:CAA37625.1; PID:q177897	
C. Species: Homo sapiens (man)	
C. Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000	
C. Accession: A37040; S24595	
P. For nastri, D.; Chirini, B.; Taroni, P.; Clementi, F.	
P. Minovilovic, M.; Ross, A.D.	
P. Neurosci. Lett. 111, 351-356, 1990	
P. Title: Molecular cloning of human neuronal nicotinic receptor alpha-3-subunit.	
P. Reference number: A37040; MUID:90245296; PMID:2336208	
P. Accession: A37040	
P. Molecule type: mRNA	
P. Residues: 1-502 <WIL>	
P. Cross-references: EMBL:X52239; PIDN:AAAC8476-1; PID:q177898	

C:Superfamily: acetylcholine receptor	Best Local Similarity 38.9%; Pred. No. 1.3e-15;	Mismatches 89; Indels 163; Gaps 5;	Query Match 37.2%; Score 982.5; DB 2; Length 502;
C:Keywords: neurotransmitter receptor; transmembrane protein	Best Local Similarity 38.9%; Pred. No. 1.3e-15;	Mismatches 89; Indels 163; Gaps 5;	
F:1-28/Domain: signal sequence #status predicted <SIG>	Best Local Similarity 38.9%; Pred. No. 1.3e-15;	Mismatches 89; Indels 163; Gaps 5;	
F:29-502/Product: nicotinic acetylcholine receptor alpha-3 chain #status predicted <MAT>	Best Local Similarity 38.9%; Pred. No. 1.3e-15;	Mismatches 89; Indels 163; Gaps 5;	
Qy 8 LALLALLPSEQGPHEPKRLLNLLANNTLERPVANESEPLEVRFLCTLQOIDVDEDKNQ 67	Db 17 LLGLLPLPVARASEEERFLERFLDYNEIRPVAVNSDPTVILQMSQLVKVDENQ 76		
Qy 68 LLITINLWLNLNDNLNRNDSEYGGVVKDILRITPNKLWKPDPVLMYNSADEGFDGTYQTNV 127	Db 77 IMETINLWLKLQIWNDYKLKNPNSKGCGAEMKVRPAKIKWEDIVLNNAVGDFQVTTRKTA 136		
Qy 128 VVRSGGSCLYVPPG1LFKSTCKMDLAWEPEDDQHCMKFGSMWTYDQDNOLDLYKDEAGGDL 187	Db 137 LLKTYGEVTTWIPPAFKSSCKIDVYTFPFQXNCNTMKFGWSYDRAKIDLVLG-SMMNL 195		
Qy 188 SDFITNGEWYLIGMCKNNTITYACCEPEPYDVDTIMIRRRTLYFFNLTVPVCYLISM 247	Db 196 KDWSEGVAIIKAGYKDHAKYKINGCCEYDPTTYSLSYSLRLPFTYINLIPCLLISFL 255		
Qy 248 ALLGFTLPLPPDSGKEKLTGLVTTILLSLTVFVNLAETLPQVSDAIPPLGTYENCIMPMVASS 307	Db 256 TVLTVYLP PSDCGEKTLCVSVLSTVLLVITEPSTSLSVILPIGEYLFTMVFVTL 315		
Qy 308 VVLTYVVLVNNYHHTADITHMPWQTKSVEQLOWLPWLMSPRGKKLTKRTIMMNTRRELE 367	Db 316 IVTIVFVNVHYRPTTHMPSWVTTVFLNLPRTMFTRP----- 356		
Qy 368 LKERSSKSLLANVLDIDDDERHGKPPPPNSTASTGNL----- 408	Db 357 -----TSNEQNAQQKPRPLYGAELSNCFSAESESSCKEGYPQCQDMCGY 401		
Qy 409 -----IERTDFRSVTPRSTMEDVGG--GLGSHSHRELHLIRELOEFTIARMKKDAEEAEI 461	Db 402 CHARRIKISNSFSANLTSSSESSVDAVSVSLSALSEIKEIAQSVKVIAENNMKAQNEAKEI 461		
Qy 462 ISDWKFAAMVYDRECFLYFTLTIATVAVL 493	Db 462 QDDWKRYVANVDIRFLWVFTLVCITGTAGLFL 493		
RESULT 13			
S60589 acetylcholine receptor alpha chain precursor - bovine			
C;Species: Bos primigenius taurus (cattle)			
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999			
C;Accession: S60589			
R;Criado, M.; Alano, L.; Navarro, A.			
Neurochem. Res. 17, 281-287, 1992			
A;Title: Primary structure of an agonist binding subunit of the nicotinic acetylcholine			
A;Reference number: S60589; MUID:92319195; PMID:1620271			
A;Accession: S60589			
A;Status: preliminary			
A;Molecule type: mRNA			
C;Residues: 1-495 <CRI>			
A;Cross references: EMBL:X57032; NID:9297762; PID:CAR40348.1; PID:9297763			
C;Superfamily: acetylcholine receptor			
C;Keywords: neurotransmitter receptor			
F:1-21/Domain: signal sequence #status predicted <SIG>			
F:22-495/Product: acetylcholine receptor alpha chain #status predicted <MAT>			
Qy 5 LAALALLALPVSEGOGPHEKRLNLLANNTLERPVANESEPLEVRFLCTLQOIDVDE 64	Db 7 LRLLLLPLPVASTSDAEEHRLFEELDFNEIRPVAVNSDPTVILQFEYSMSQVVKVD 66		

QY	65	KNQLLITNIWLSLEWDYNLRWNDESEYGGVKDLRLTIPNKLUWPKDVLMLNSADEGGFDGTYQ	124
Db	67	VNQIMETNWLQIWNNDYKLKWNPDPYDGBEFMRPAEKIDVLYNNADGFQDDK	126
QY	125	TNVVPSGSCLIVPGIFKFKSTCKMDIANWPEDDQACDMKFGSWYWDGKQDLDLVLEDEAG	184
Db	127	TKALKYTGEVTWPAIPSSCKIDVDTYFPFDYQNCNTMFGWSWYDKAKIDLVLIG-SS	185
QY	185	GDLSDPITNGEWYLIGMPGKRNNTITYACCPBPYDVFTFTIMIRRRTLYFFNLIVPCVLI	244
Db	186	MNIXDXYWESEWAIIKAPGYKHDKYNCCEETIPYDTSYIIRPPLFPTINLIFPLIV	245
QY	245	SSMALGETLPDSDCEKLTGVTUTLTSITVFLNIVAYETLPQVSDAIPLLGTYFCNCIMFMV	304
Db	246	SFLVPLVETLPSPDCBKVTLVLLSITVFLNIVETITSVPLIGEYLFLTMIV	305
QY	305	ASSVWLTIVVWLNKHRTADTHEMOWIKSVFLQWTFWLMSRPGK--KTRTRKTTMMNT	361
Db	306	TLSITVTEVPLVHRTPTHTMPAWKCLFLNLLPRVMEMTRPASNENGTQRPRPFYSA	365
QY	362	RMRETELKRSSKSILANVLDDDFRHHGPPNASTAQNGLGPSSIFR--TDFRRSF	418
Db	366	ELSNLNCFRIESYC-----KEGYP---CQDLCG-YCHHRKAKISNSANL	409
QY	419	VRPSTMEDYGG--GIGSHHRELHLIRELQFITARNKKADEEAEILISDWNKPAAMYVDRFC	476
Db	410	TRSSSESYDAVLSSALSASPIKEIAQSVKXIAENMKAAQNBAKEIQQDWKXVAMYVIDRIF	469
QY	477	LEVPLFTIATVAVL	493
Db	470	LWVPLVCLTGAGIFL	486
RESULT 14			
A	A24572	nicotinic acetylcholine receptor alpha-3 chain precursor - rat	
C	Species: Rattus norvegicus (Norway rat)		
C	Date: 30-Jun-1998 #sequence_revision 30-Jun-1998 #text_change 08-Nov-1996		
C	Accession: A24572		
R	Boulter, J.; Evans, K.; Goldman, D.; Martin, G.; Treco, D.; Heinemann, S.; P		
N	Nature 319, 368-374, 1986		
A	Title: Isolation of a cDNA clone coding for a possible neural nicotinic acetylcholine receptor. PMID:86118671; PMID:3753746		
A	Reference number: A24572;		
A	Accession: A24572;		
A	Molecule type: mRNA		
C	Residues: 1-499 <BOU>		
C	Superfamily: acetylcholine receptor		
C	Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic		
F	1-25/Domain: signal sequence #status predicted <SIG>		
F	26-499/Product: nicotinic acetylcholine receptor alpha chain #status predict		
Query Match	36.8%	Score 970.5; DB 2; Length 499;	
Best Local Similarity	39.6%	Pred. NO. 1.3e-74; Missmatches 180; Indels 33; Gaps 7;	
Matches	199;	Conservative 91; Mis matches 180; Indels 33; Gaps 7;	
QY	3	PMLAAALLALPVESEQGPHEKRLINALLANYNTLERYPANESEPLEVRFGLTQOIDV	62
Db	9	PLSMMLVMLLPPASASDAEHRLFQYLFDYNEIIRPYANVSHVVIQEVSMSQLVKY	68
QY	63	DEKNQQLITNWLSEWNDYLNRLDSEYGGVKDLRLTIPNKLUWPKDVLMLNSADGFQVD	122
Db	69	DEVNQIMETNWLQIWNNDYKLKPKSDYQGVEMRVPAEKIDVLYNNADGFQVD	128
QY	123	YCTNVVVRSGGSCLIVYPPGIFKSTCKMDIAWFPEPDQHCDMKEGSWTGYGNOLDLVLKDE	182
Db	129	DKTKALLXKTGEVWIPPAFKSKCIDTYFPDYQNCNTMKGFSWYDKAKIDLVLIG-	187
QY	183	AGGDSDFITNGEMYLIGMPGKONTITYACCPBPYDVFTTIMIRRRTLYFFNLIVPCV	242
Db	188	SSMLKLDYKWESEGAIIKAPGYKHEIYQNCCEBTYDITSLYFRRLPLFYTNLJIPCL	247
QY	243	LISSMALLGFTLPDSDGEKLTGILLSLTVEFLNVLARTLPQVSDAIPLGLTYNCIMF	303



Scoring table:	BLOSUM62					
Gapop:	10.0 , Gapext 0.5					
Searched:	141681 seqs, 52070155 residues					
Total number of hits satisfying chosen parameters:	141681					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing:	Minimum Match 100% Maximum Match 100% Listing First 45 summaries					
Database :	Swissprot_42:*					
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES						
Result No.	Score	Query	Match	Length	DB ID	Description
-	-	-	-	-	-	-
1	1258.5	47.6	502	1	ACH7_HUMAN	P3644 homo sapien
2	1255.5	47.6	502	1	ACH7_MOUSE	P49582 mus musculus
3	1253	47.5	502	1	ACH7_CHICK	P2270 gallus gallus
4	1240.5	47.2	502	1	ACH7_RAT	P09411 rattus norvegicus
5	1240.5	47.0	499	1	ACH7_BOVIN	P54131 bos taurus
6	1237.5	46.9	498	1	ACHL_GAEL	P48380 caenorhabditis elegans
7	989.5	37.5	503	1	ACH3_HUMAN	P32297 homo sapien
8	977.5	37.0	499	1	ACH3_RAT	P04577 rattus norvegicus
9	970.5	36.8	495	1	ACH3_BOVIN	Q07963 bos taurus
10	964.5	36.5	567	1	ACH1_DROME	P09478 drosophila melanogaster
11	948.5	35.9	496	1	ACH3_CHICK	P09481 gallus gallus
12	946.5	35.9	516	1	ACH1_MANSE	P91166 manduca sexta
13	944	35.8	557	1	ACH1_SCHGR	P23614 schistocerca gregaria
14	943	35.7	576	1	ACH2_DROME	P17444 drosophila melanogaster
15	933	35.3	494	1	ACH6_HUMAN	Q15255 homo sapien
16	924	35.0	528	1	ACH2_CHICK	P09480 gallus gallus
17	922.5	34.9	529	1	ACH2_CHICK	Q15222 homo sapien
18	919.5	34.8	512	1	ACH3_CARAU	P18845 carassius auratus
19	917	34.7	511	1	ACH2_RAT	P12489 rattus norvegicus
20	915.5	34.7	494	1	ACH6_CHICK	P49581 gallus gallus
21	914.5	34.6	493	1	ACH6_RAT	P43143 rattus norvegicus
22	910.5	34.5	495	1	ACHP_RAT	P12492 rattus norvegicus
23	908.5	34.4	519	1	ACH4_DROME	P25162 drosophila melanogaster
24	906	34.3	457	1	ACHA_BOVIN	P02709 bos taurus
25	900	34.1	521	1	ACH3_DROME	P04755 drosophila melanogaster
26	899.5	34.1	500	1	ACHN_RAT	P12490 rattus norvegicus
27	897.5	34.0	627	1	ACH4_HUMAN	P43681 homo sapien
28	896	33.9	456	1	ACHA_CHICK	P09479 gallus gallus
29	895	33.9	502	1	ACHN_HUMAN	P17787 homo sapien
30	891	33.8	622	1	ACH4_CHICK	P09482 gallus gallus
31	890.5	33.7	629	1	ACH4_MOUSE	P07074 mus musculus
32	890	33.7	457	1	ACHA_RAT	P25108 rattus norvegicus
33	890	33.7	470	1	ACHP_CHICK	P26153 gallus gallus

Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

[7] SEQUENCE OF 17-502 FROM N.A.  
TISSUE=Brain;  
RC Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T.,  
RA Lee J., Tian J., Giordano T.;  
RT "Cloning and sequence of the human a7 nicotinic acetylcholine receptor.",  
RL Drug Dev. Res. 30:252-256(1993).  
RN [8] SEQUENCE OF 24-502 FROM N.A.  
RC TISSUE=Retina;  
RX MEDLINE=9445214; PubMed=8188270;  
RA Chini R., Raimondi E., Elroyhen A.B., Morallli D., Balzaretti M.,  
RA Heinemann S.F.;  
RT "Molecular cloning and chromosomal localization of the human alpha 7-nicotinic receptor subunit gene (CHRNA7)." ;  
RL Genomics 19:379-381(1994).  
RN [9] SEQUENCE OF 118-129 FROM N.A.  
BX MEDLINE=21818878; PubMed=11829490;  
RA Riley B., Williamson M., Collier D., Wilkie H., Makoff A.;  
RT "A 3-Mb map of a large segmental duplication overlapping the alpha 7-nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14." ;  
RL Genomics 79:197-209(2002).  
RN [10] MASS SPECTROMETRY.  
RC TISSUE=Breast cancer;  
RX MEDLINE=81829512; PubMed=11840567;  
RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,  
RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,  
RA Zelish M.J.;  
RT "Cluster analysis of an extensive human breast cancer cell line protein expression map database." ;  
RT Proteomics 2:212-223(2002).  
CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma membrane.  
CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-bungarotoxin. The structure is probably pentameric (By similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- MASS SPECTROMETRY: MW=54157.68; METID=MEIDI.  
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.  
CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. There is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; CBA49778.1; -.  
DR EMBL; U40583; AAA83561; -.  
DR EMBL; U62436; AAB4014.1; -.  
DR EMBL; Y08420; CBA69697.1; -.  
DR EMBL; AF385585; AAK68111.1; -.  
DR EMBL; L25827; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; 223141; CAA80672.1; -.  
DR EMBL; AF332758; AAK19515.1; -.  
DR PIR; G02259; G02259.  
DR PIR; I37105; ACUHA7.  
DR Gene; HGNC:1965; CHRNA7.  
DR MIM; 118511; -.  
DR GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. . . ; TAS.  
DR GO; GO:0015464; F:acetylcholine receptor activity; TAS.  
DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . . ; TAS.  
DR GO; GO:0006810; P:activation of MAPK; TAS.  
DR InterPro; IPR000209; Neu\_channel\_memb.  
DR InterPro; IPR000202; Neu\_channel\_LBD.

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DR MIM; 118511; -.  
DR GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. . . ; TAS.  
DR GO; GO:0015464; F:acetylcholine receptor activity; TAS.  
DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . . ; TAS.  
DR GO; GO:0006810; P:activation of MAPK; TAS.  
DR InterPro; IPR000209; Neu\_channel\_memb.  
DR InterPro; IPR000202; Neu\_channel\_LBD.

InterPro; IPR006201; Neur\_channel\_1.  
DR Pfam; PF02331; Neur Chan LBD; 1.  
DR Pfam; PF00932; Neu-Chan\_memb; 1.  
DR PRINTS; PR00252; NRIONCHANNEL.  
DR TIGRFAMS; TIGR00860; LIGC\_1.  
DR PROSITE; PS00236; NEUROTR\_ION CHANNEL; 1.  
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family.  
FT SIGNAL 1 22 BY SIMILARITY.  
FT CHAIN 23 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,  
EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 23 230 ALPHA-7 CHAIN.  
FT TRANSEM 231 255 EXTRACELLULAR (POTENTIAL).  
FT TRANSEM 262 280 POTENTIAL.  
FT DOMAIN 318 469 CYTOPLASMIC (POTENTIAL).  
FT TRANSEM 470 490 POTENTIAL.  
FT DISUFID 150 164 BY SIMILARITY.  
FT DISUFID 212 213 ASSOCIATED WITH RECEPTOR ACTIVATION  
(BY SIMILARITY).  
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . . ) (POTENTIAL).  
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . . ) (POTENTIAL).  
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . . ) (POTENTIAL).  
FT CONFLICT 11 11 A -> G (IN REF. 1 AND 7).  
FT CONFLICT 58 58 S -> N (IN REF. 2 AND 6).  
FT CONFLICT 134 134 S -> P (IN REF. 2 AND 6).  
FT CONFLICT 364 364 C -> S (IN REF. 8).  
FT CONFLICT 375 375 A -> G (IN REF. 1).  
FT CONFLICT 409 413 RMAC8 -> AWPAP (IN REF. 8).  
SQ SEQUENCE 502 AA; D94B3A432EA0E42 CRC64;  
SQ SEQUENCE 502 AA; D94B3A432EA0E42 CRC64;

Query Match 4 7.7% Score 1258.5; DB 1; Length 502;  
Best Local Similarity 48.6%; Pred. No. 6.3e-102; Gaps 7;  
Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;  
QY 8 LALLA-LLPVSEQQGPHEKRLLNANLYNTLERPVANESEPLEVREGFLTQLQIIVDEKN 66  
Db 10 LALAASLLHVSLSQGEFQRKLYKELVVNNPLRPVANDSQBTLVTFESLQLQMDVDEKN 69  
QY 67 QLLITNNIWLSEWNDYNLRANDSEYGGVXDLRITPNKLWEPDVLYNSADEGFDTGYQTN 126  
Db 70 QVLITNNIWLQMSWTDYLNQVSEYEGVKTVPFDQIQWPKDILLYNSADERFDATFHNT 129  
Db 127 VVRSSGSCCLVPPGLFKSTKMDIAWFPDDQHCDMKFQSWTYDNQNDLVLDEAGGD 186  
QY 130 VLVNSSGHQCYIYDWRWFPPVQHCKLKFGSSWYSGVWSLQDLOMCE --AD 186  
QY 187 LSDFITNGEWYLGMGPQKONTITYACCPPEPYVDFTTIMIRRLLYYFFNLIVPCVLISS 246  
Db 187 ISGYTENGDWLVLFGKRSERFYECCKEKPVDFTVIMRRLLYYGLNLIPCVLISSA 246  
QY 247 MALIGGTTLPPSGEKLTGTVLISLTSVTFUNLVAAETLPQSDAIIPLGTYFNCLNMVAS 306  
Db 247 LALLYFLPADSGEKSISLGTVLISLTSVFMVLVAETMPATSVDVPLIAQETASTMLVGL 306  
QY 307 SVVLTIVLNHRTADITHEMPQWIKSVFLQWLPWILMRSPGKKITRKIMMNTRMREL 366  
Db 307 SVVVTIVLQYTHHHDGGKMPKWTIVLNNCAFLRMRCPGEKVRPACQHKQRRCSL 366  
QY 367 ELKERSKSLLIANVLDIDDDFRHGPPPNNSTASTGNL-----GPGC 407  
Db 367 ASVEMSAVA-----PPP--ASNGNLLYIGFRGLDGVHCVPTPSGSVVVC 407  
QY 408 SIFRTDFRRSFVRPSSTMEDV-GGGGGSHEHLTRELQFTARMKKDAEEAELJSWD 465  
Db 408 G-----RMACTPDEHLHGGOPPEGDDLAKILEEVRYIANFRCODESEAVCSEW 460  
QY 466 KFAAMVYDRCFLFVFLPTLTIAVAVLSAPHII 499  
Db 461 KFAACVYDRCFLMMAFSVFTLICTGTIMSAENFV 494

ACH7_MOUSE	STANDARD;	PRT;	502 AA.	
ID P49582;				
AC				
DT 01-FEB-1996 (Rel. 33, Created)				
DT 01-FEB-1996 (Rel. 33, Last sequence update)				
DT 28-FEB-2003 (Rel. 41, Last annotation update)				
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.				
GN CHRNA7.				
OS Mus musculus (Mouse).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.				
NCBI_TaxID=10090;				
RN [1]				
RP FROM N.A.				
RC STRAIN=BALB/C; ISSUE=Brain;				
RX MEDLINE=95324936; PubMed=7601470;				
RA Orr-Urtreger A., Seldin M.F., Baldini A., Beaudet A.L.;				
RT "Cloning and mapping of the mouse alpha 7-neuronal nicotinic acetylcholine receptor."				
RT Genomics 26:399-402 (1995).				
-!_ FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma membrane.				
-!_ SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-bungarotoxin. The structure is probably pentameric (By similarity).				
CC -!_ SUBCELLULAR LOCATION: Integral membrane protein.				
CC -!_ SIMILARITY: Belongs to the ligand-gated ionic channel family.				
CC				
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CC				
DR EMBL; I37663; AAC42053.1; -.				
DR FIR; A57175; A57175.				
DR MGD; MG9779; Charna7.				
DR InterPro; IPR006029; Neu_channel_memb.				
DR InterPro; IPR006202; Neu_chan_LBD.				
DR InterPro; IPR006201; Neu_chan_EI.				
DR Pfam; PF02931; Neu_chan_ITD; 1.				
DR Pfam; PF02932; Neu_chan_memb; 1.				
DR PRINTS; PR00252; NTRIONCHANNEL.				
DR PROSITE; PS00036; NEUROTR_ION_CHANNEL_1.				
DR Transmembrane; Ionic_channel; Glycoprotein; Signal;				
KW Transmembrane; Multigene family				
FT SIGNAL 1 22 BY SIMILARITY.				
FT CHAIN 23 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,				
FT DOMAIN 23 230 ALPHA-7 CHAIN.				
FT TRANSMEM 231 255 EXTRACELLULAR (POTENTIAL).				
FT TRANSMEM 262 280 POTENTIAL.				
FT TRANSMEM 296 317 CYTOPLASMIC (POTENTIAL).				
FT DOMAIN 318 469 POTENTIAL.				
FT TRANSMEM 470 490 BY SIMILARITY.				
FT DISULFID 150 164 ASSOCIATED WITH RECEPTOR ACTIVATION				
FT DISULFID 212 213 (BY SIMILARITY).				
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).				
FT CARBOHYD 90 90 N-LINKED (GLCNAC. .) (POTENTIAL).				
FT CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).				
SQ SEQUENCE 502 AA; 56631 MW; C9312E5226120E3 CRC44;				
Query Match 47.6% Score 1255.5; DB 1; Length 502;				
Best Local Similarity 49.6% Pred. No. 1.e-10; Mismatches 14%; Indels 27; Gaps 7;				
Matches 249; Conservative 78; STRAIN=White_Leighorn; TISSUE=Erythrocyte;				
RX MEDLINE=930499204; PubMed=1425587;				
RA Matter-Sadzinski L., Hernandez M.C., Roztocil T., Ballivet M.,				
[3]				

RA Matter J.M.; "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor promoter develops during morphogenesis of the central nervous system.", RT R. L. EMBO J. 11:4529-4538(1992). [4]

RN SEQUENCE OF 24-47.

RP TISSUE=Brain; RX MEDLINE=92270494; PubMed=3860855;

RA Conti-Tronconi B.M., Dunn S.M.J., Bernard E.A., Dolly J.O., Lai F.A., Ray N., Raftery M.A.; "Brain and muscle nicotinic acetylcholine receptors are different but homologous proteins."; Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985). [5]

RN MUTAGENESIS OF LEU-270. RP MEDLINE=93049722; PubMed=1719423;

RA Recab F., Bertrand D., Galzi J.-L., Devilliers-Thiery A., Mulle C., Hussy N., Bertrand S., Ballivet M., Changeux J.-P.; "Mutations in the channel domain alter desensitization of a neuronal nicotinic receptor"; Nature 355:846-849(1991). [6]

RN MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC. RX MEDLINE=93024917; PubMed=1383829;

RA Changaux J.-P., Devilliers-Thiery A., Hussy N., Bertrand S., Galzi J.-L., Bertrand D.; "Mutations in the channel domain of a neuronal nicotinic receptor convert ion selectivity from cationic to anionic."; RNL 359:500-505(1992).

RC FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma membrane. It forms a homo-oligomeric channel blocked by alpha-bungarotoxin. The structure is probably pentameric (By similarity).

CC -!- DEVELOPMENTAL\_STAGE: Alpha-7 transcripts transiently accumulate in the developing optic tectum between E5 and E16.

CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.

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DR EMBL; X52395; CAA36543.1; -.

DR EMBL; X68246; CAA48317.1; -.

DR PIR; JN0113; JN0113.

DR PDB; 1KLC; 17-APR-02.

DR PDB; 1KL8; 17-APR-02.

DR InterPro; IPR006029; Neu channel memb.

DR InterPro; IPR006202; Neur chan LBD.

DR InterPro; IPR006201; Neur chan LBD.

PFam; PF02931; Neur chan LBD; 1.

DR PRINTS; PR00255; NRIONCHANNEL.

DR TIGRFams; TIGR00860; LIC; 1.

KW Post-synaptic membrane; Ionic Channel; Glycoprotein; Signal; KW Transmembrane; Multigene family; 3D-structure.

FT SIGNAL 1 23

FT CHAIN 24 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN.

FT DOMAIN 24 230 EXTRACELLULAR.

FT TRANSMEM 231 255

FT TRANSMEM 262 280

FT TRANSMEM 296 317

---

FT DOMAIN 318 469 CYTOPLASMIC.

FT TRANSMEM 470 490 BY SIMILARITY ASSOCIATED WITH RECEPTOR ACTIVATION

FT DISULFID 150 164 (BY SIMILARITY).

FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT MITOGEN 270 270 L-S-T. SUPPRESSES INHIBITION BY THE OPEN-CHANNEL BLOCKER QX-222.

FT CONFLICT 26 27 QR (IN REF. 3).

SQ SEQUENCE 502 AA; 56946 MW; 572325D4309AD2FD CRC64;

Query Match 4 / 5%; Score 1253; Length 502;

Best Local Similarity 48.8%; Pred. No. 1. 9e-101;

Matches 250; Conservative 81; Mismatches 145; Indels 36; Gaps 8;

QY 2 APMLAALIALLLPVSEQQGPHEKRILNALLANYNTLERPVANEESEPLEVRFGLTLQOID 61

Db 5 ALMLWLAAGLVLRESLQGEFQRKLYKEKKRNPLVRANDSOPLTVFTFLSLMQIMD 64

QY 62 VDEKNQLLTNIWLSLEWDNDYLNRLNDSEGGVQDLRITPNKLWKPDLUMNSADEGFDG 121

Db 65 VDEKNQLLTNIWLSQMLQMYWTHYLQMVNLNVSETPGVNMRVFPDGLVNPDPDILYNSADERFDA 124

QY 122 TYQTNVNVVRSSGSCSLLVPPGTFKSTCKRMIDTAWFPEFDQHCDMKFGSWTYDGNQLDLVLKD 181

Db 125 TFHTINVLNVSNSGHQCQLPPGTFKSSCCYIDTRWFPPDVQCNLKFSSWTGWSLQMQE 184

QY 182 EAGGDLSDFFTGNGEWYLIGMPGKNTITYACCPEPYKVDYFTIMIRRLLYYFENLIVPC 241

Db 185 --ADISGYLSNGENDLVLGPGRTESFYBCKEPPDPDITFVMMRRTLLYYGLNLIPC 241

QY 242 VLISSMALLGFTLPDGSGEKLTGNTLISLTFLVNLVAETLPQVSDAIPLGLTYFCNCIM 301

Db 242 VLISSMALLVFLPADSGEKLSLGTIVLSSLTFLVNLVAIMPATSDSVLIAQFASTM 301

QY 302 FMVASSVLLTVVVVNYHRTADIHMPQWIKSVFQLWLPMLRRSRPGKLTTRKTMNT 361

Db 302 IIVGLSVVTTVIVLQYHHPDGGCOPKWTWVLLNWCAFWLMLRCPGDKEVKPACQHQKQ 361

QY 362 RMRELELKERSKS ---LLANVLDIDDDPR ---HGPPPNNSTASTGNLNGLPGCSIFRT 412

Db 362 RRCSSLSSMENNNTVSGQCSNGNMLYI --GFRGLDGVHCTPTDSGVICGRM--TCS--- 413

QY 413 DFRRSFVRPSSTMEDVGGH(GSHH---REIHLILRELQFTARNKKAKADEAELISDWKF 467

Db 414 -----PTEBENL---LHSQHPSSEGDPDIAKLEVERYTANFRQDDEBEAICNEWKP 462

QY 468 AAMVYDVRFCFLFVPTLTITAVVLLSAPHII 499

Db 463 AASVYDVRCLMMAFSVTIICITGILMSAPNFV 494

RESULT 4

ACH7 RAT STANDARD; PRT; 502 AA.

ID AC005941; DT 01-FEB-1994 (Rel. 28, Created)

DE DT 01-FEB-1994 (Rel. 28, Last sequence update)

DE DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.

GN CHRNA7 OR ACRA7.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.

NCBI TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=33147931; PubMed=7678857;

RA Seguela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.;

RT "Molecular cloning, functional properties, and distribution of rat



QY	DR	EMBL; X93604; QAA63802_1.	
InterPro;	IPR06029;	Neur. channel memb.	
InterPro;	IPR06020;	Neur. chan. LBD.	
InterPro;	IPR06201;	Neur. -channel	
PRAM;	PF02931;	Neur. chan. LBD;	1.
PRAM;	PF02932;	Neur. chan. memb;	1.
PRINTS;	PR00252;	NRONCHANNEL.	
TIGRFAMs;	TIGR00860;	LIC;	1.
PROSITE;	PS00236;	NEURO76: NEURO76 ION CHANNEL;	1.
KW	Postsynaptic membrane; Ionic Channel; Glycoprotein; Signal;		
KW	Transmembrane; Multigene family; Alternative splicing.		
SIGNAL	1	BY SIMILARITY.	
CHAIN	20	499	
FT	DOMAIN	20	227
FT	TRANSEM	228	252
FT	TRANSEM	259	277
FT	TRANSEM	293	314
FT	DOMAIN	315	466
FT	TRANSEM	467	487
FT	DISULFID	147	161
FT	DISULFID	209	210
CARBHYD	43	43	
CARBHYD	87	87	
CARBHYD	130	130	
VARSPLIC	262	290	
SEQUENCE	499	AA;	56002 MW; AEE5D0B3820D42DS CRC64;
Query Match		47.0%	Score 1240.5; DB 1; Length 499;
Best Local Similarity		49.4%	Pred. No. 2 3e-100;
Matches	247;	Conservative	Mismatches 152; Indels 23; Gaps 6;
QY	DR	LLALA-LLPYSEQGPHEKRLLNALLANNTLRLPVAESEPLEVRFGTLTQQIIDVDEKRN 126	
QY	DRb	7 LALAA-SILHSLYSLQGEFQRKLXLYQMLQWNAESEPVKVTYRFPDGQTWKEDDLILYNSADERDTAFTEN 126	
QY	DRb	8 QLLITNIWLSLEWDNWLRLNDSEYIGCIVKQDRLRTPNKLWKPDKVLMYNSADEGFDGTQTN 126	
QY	DRb	67 QVLTTINWLSQMLWTWHDYLQWNAESEPVKVTYRFPDGQTWKEDDLILYNSADERDTAFTEN 126	
QY	DRb	67 VVRRGGSCLYVPPGTFKSTCRKDMDIAWEFPDDQHCMDKFGSWTYDGNQDLVLRD EAGGD 186	
QY	DRb	127 VLVNSSGHQCQLYQPLPGFVKSSCYIDVWRFPEDVQQCLKFGWSYGVGSLLDQNQE--AD 183	
QY	DRb	127 VLVNSSGHQCQLYQPLPGFVKSSCYIDVWRFPEDVQQCLKFGWSYGVGSLLDQNQE--AD 183	
QY	DRb	187 LSDFTINGEWYLIGMGPKGKNTITYACCPPEPYDVTFITMIRRTLYYFNLTVYFCVLISS 246	
QY	DRb	184 ISGYTPNGEDLVLGVIGRKSEKFKEPKYDVTFIVSIRRTLYYGINLLPCVLISA 243	
QY	DRb	247 MALLGFPLPDPSGEKLTGVTILLSTSTVFLNLYAETLPQVSDAIPLLGTYENCIMYMVAS 306	
QY	DRb	244 LALLIVLPLPADSGEKLSLGLTIVLLSLTVEMLIVAEIMPATSDSVPLIQLQYFASTMIVCL 303	
QY	DRb	307 SVVLTIVVLYNHHRTPDADIHEMPQWIKSVFLQWLPWIRMSRPGKKITPKTMMTRMREL 366	
QY	DRb	304 SVVVTVTIVLQYHHDPGGKMEKWTYVLLNCAWFLRMKRGSEDKYRPACQINERRCSL 363	
QY	DRb	367 ELKERS---KSLLANVLDDDD--DFRHGKPPNPNSTASTGNLPGCCSIFRTDFRRFSV 419	
QY	DRb	364 ASVENSAVAGPATNGNLLYIGRGLDTMHCAPTPDGCVYGRV--ACSPSPTHDEHLHLHRS 421	
QY	DRb	420 RPSTMEDVGGGLGSHREHLTLIREQFITAEMKADEAEELISDWKPAAMVYDRFCLFV 479	

FT	CARBOHYD	93	93	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SQ	SEQUENCE	498 AA;	57169 MW;	E463ABB409FA82	CRC64;
Query Match	Score	1237.5;	DB 1;	Length	498;
Best Local Similarity	46.9%;	Pred. No.	4..3e-100;		
Matches 245;	Conservative 80;	Mismatches	140;	Indels	51;
		Gaps	9;		
QY	2	APMLAAALLLPVSEQQGPHEKRLLNALLANNTLERRPVANESEPLEVRFGTILQLQID	61		
Db	15	APTIGSL-----QERPTYLIMRANTNNLERPAHSESEPTVHLKVALQQID	61	RN	[4]
Db	62	VDEKNOLLITNTWLSLENDYNLRNWDSEBYGYKDLRTPNKLWKPDVLYMNSADBEFDG	121	RN	SEQUENCE FROM N.A. (ISOFORM 1).
QY	62	:   :       :   :     :   :     :   :     :   :     :   :     :   :	121	RX	MEDLINE=97062879; PubMed=906617;
Db	62	VDEKNQVVYVNAMLDYTNDYLNWVDAKEGNTIDVREPAAGKWKPDVLYMNSVDNFDS	121	RA	RA
QY	122	TYQINVVVRSSGSSLVYPGIFKSTCKNDIADWFDDOHDCKMFKGSMTYDGNDLIVKD	181	RT	"Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SY5Y and/or IMR-32.";
Db	122	TYQTINMITYSTGLYVHWVPGFKISCKDIDQWPFDEOKCFFKGSMWTVGYKLDRQ	179	RT	RT
QY	182	EAGG-DLSDFITNGEYLIGMPGKRNITTYACCPPEPYDVTETIMIRRATYYFENLIVP	240	RL	RL
Db	180	ARGFDISETYISGEWAALPLTVVERNEKEYDCCEPEVDHFVLMHMRRTLYGENLIMP	239	RN	RN
QY	241	CYLISSMALIGLTFLPPDSGEKLTIGLTILSITLVNLIVAYETLPLQVSDAIPLGTYFNCI	300	RP	SEQUENCE FROM N.A. AND VARIANT LEU-21 INS.
Db	240	CILTLTMFLGFLPPDAEGKLTQITVLISICFFLTSVSESPTEAVPLGIFFC	299	RX	MEDLINE=99118870; PubMed=921897;
QY	301	MFVMASSVYLTVVLYNTHRTADLHEMPWIKSVFLQWLPWLIRMSRPGKJTRKTI-M	358	RA	RA
Db	300	MIVVTAStVTFVYLNLYHRTPTEDMGWPTRNLWLPWLIRMKRGHNLYASLPSL	359	RA	Lev-Leiman E.; Bercovich D.; Xu W.; Stockton D.W.; Beaudet A.L.; RT
QY	359	MNTRMRELELKERSKSLLANL-----IDDDFRHGCPPPNSTASTCGNLGPCCS	408	RT	"The structures of the human beta4 nAChR gene and polymorphisms in CRNA3 and CRNB4.";
Db	360	FSTK-----PNHHSESLRNKDNNEHSLSTRANSFDAQRNLXOYIMFQSNSNLTSQG-S	412	RL	RT
QY	409	IERTDFRSFVRPSTMEDVGGGLGSHIRE----IHLIRELOFITARMKKADEAEALL	463	RN	RN
Db	413	-----PSTMISNGTTDVSSQATLILHRYELKIVTRMIEGDKEEQACN	461	RC	SEQUENCE FROM N.A. (ISOFORM 2).
QY	464	DWKPAAMYTDVRFCLFVFTIFTIATAVILSAPHII	499	RT	RT
Db	462	NNWPAAMYTDVRLCYLFVFTIIVSTIGFWSAFYLV	497	RT	RT
RESULT 7				RT	RT
ACB3_HUMAN	ID	Q15823; Q96RH3 ; Q99553 ; Q9BQ33 ;	PRT;	503 AA.	RT
AC	P32297	01-27, Created)			RT
DT	01-OCT-1993	(Rel.			RT
DT	01-OCT-2003	(Rel.	35, Last sequence update)		RT
DE		42, Last annotation update)			RT
GN					RT
CHRNA3					RT
Homo sapiens (Human).					RT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.					RT
OX	NCBI TAXID=9606;				RT
RN					RT
RP					RT
SEQUENCE FROM N.A.					RT
RX	MEDLINE=90245296; PubMed=2336208;				RT
RA	Fornasari D., Chirri B., Taroni P., Clementi F.;				RT
RT	"Molecular cloning of human neuronal nicotinic receptor alpha 3-subunit."				RT
RT	Neurosci. Lett. 111:351-356(1990).				RT
RJ					RT
RN					RT
SEQUENCE FROM N.A.					RT
RP	SEQUENCE FROM N.A. (ISOFORM 1).				RT
RC	TISSUE=Thymus;				RT
RX	MEDLINE=91114756; PubMed=199896;				RT
RA	Mihovilovic M., Rosse A.D.:				RT
RT	"Expression of mRNAs in human thymus coding for the alpha 3 subunit of a neuronal acetylcholine receptor."				RT
RL	Exp. Neurol. 111:175-180(1991).				RT
RN					RT

-!- SUBCELLULAR LOCATION: Integral membrane protein.  
 -!- ALTERNATIVE PRODUCTS:  
 Event=Alternative splicing; Named isoforms=2;  
 Name=;;  
 IsoId=p32297-1; Sequence=Displayed;

Name=2;  
 IsoId=p32297-2; Sequence=vSP\_00073;

Note=No experimental confirmation available; channel family;  
 SIMILARITY: Belongs to the ligand-gated ionic channel family.

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EMBL; M80383; AACBA476\_1; -  
 EMBL; U62432; AAA5942\_1; -  
 EMBL; U62432; Y08418; CAA63695\_1; -  
 EMBL; AJ007783; CAA07682\_1; -  
 EMBL; AJ007784; CAA07682\_1; JOINED.  
 EMBL; AJ007785; CAA07682\_1; JOINED.  
 EMBL; AJ007786; CAA07682\_1; JOINED.  
 EMBL; AJ007787; CAA07682\_1; JOINED.  
 DR EMBL; BC001642; AAH01642\_1; -  
 DR EMBL; BC002996; AAH02996\_1; -  
 DR EMBL; BC005013; AAH00513\_1; -  
 EMBL; AFJ85584; AAJ68110\_1; -  
 DR EMBL; X53359; CAJ37625\_1; -  
 PIR; A37040; A37040\_1; -  
 DR PIR; A53956; A53956\_1;  
 DR Gene; HGNC:1557; CHRNA3.  
 DR MIM:118503; -  
 DR GO:0005892; C:nicotinic acetylcholine-gated receptor Chan. . . ; TAS.  
 DR GO; GO:0015464; F:acetylcholine receptor activity; TAS.  
 DR GO; GO:004889; F:nicotinic acetylcholine-activated cation se. . . ; TAS.  
 DR GO; GO:0005215; F:transporter activity; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR006029; Neu\_channel memb.  
 DR InterPro; IPR006202; Neur\_chan\_LBD.  
 DR InterPro; IPR006201; Neur\_channel.  
 DR Pfam; PF02931; Neu chan LBD; 1.  
 DR PRINTS; PR00252; NEUR\_CHANMEL.  
 DR TIGRFAM; TIGR00860; LIC; 1.  
 PROSITE; PS00236; NEUROPI\_ION CHANNEL; 1.  
 Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family; Alternative splicing; Polymorphism.  
 KW SIGNAL 1 29  
 PT CHAIN 30 503  
 DOMAIN 30 238  
 PT TRANSMEM 239 263  
 PT TRANSMEM 271 289  
 PT DOMAIN 305 326  
 PT TRANSMEM 327 475  
 PT DISULFID 476 495  
 PT DISULFID 157 171  
 PT 221 222  
 PT VARIANT 21 21  
 PT CONFLICT 53 53  
 PT CONFLICT 170 170  
 PT VARPLIC 1 5  
 PT CONFLICT 11 14  
 PT CONFLICT 100 100

FT CONFLICT 132 133 DD -> TT (IN REF. 1).  
 FT CONFLICT 235 235 I -> S (IN REF. 1).  
 FT CONFLICT 430 430 L -> V (IN REF. 1).  
 SEQUENCE 503 AA; 57309 MW; BA9BBC5D1ABC7D6 CRC64;

Query Match 37.5%; Score 989.5; DB 1; Length 503;  
 Best Local Similarity 38.5%; Pred. No. 1.9e-78; Mismatches 166; Indels 61; Gaps 5;

Matches 200; Conservative 92; MisMatches 166; Indels 61; Gaps 5;

Qy 1 MAPMIAALALLLPVSEQPHERKLLNALLANTLERPVANSEPLEVRFGLTQQII 60  
 Db 11 LSPRULLLSSLLEVAVASEAHLERFLERDFNELLIREVANSDPVTHFEVSMSQLV 70  
 Qy 61 DVDEQNQLLITINNLISLEWNDYLNWNSDSEYGGDRITPNKWRKPDLMYNSADEGFD 120  
 Db 71 KVDEYNQIMEINLWKQIWDYKLNWPSDGGAEFMRVPAQKWKPDIVLYNAVGDFQ 130  
 Qy 121 GTYQTNNVVVRSGGSCLYVPPGIFKSTCKMDIAWMFPDDOHCDMKRGFSWTYDGNCQDVLK 180  
 Db 131 VDDKPKALLKXTGEVWIWPAIKFSKCKDVTYFPDYQNCTMKGWSYSDKAICDVLJ 190  
 Qy 181 DEAGGDLSDFITNGWLYLGMGPQKNTTYACCP CPPYDVTFIMRRRTLYFFENLIVP 240  
 Db 191 G-SRNLLKDQWSEGWAIKPGYKHDIXNCCB1YDPTYSYLRLPLFYTNLIP 249  
 Qy 241 CVLISSMALLIGFTLPDSGEGKLITGVTLTFLVNLVAYETLPOVSDAIPPLGTYFNCL 300  
 Db 250 CLLISFLTVYFYLPSDCGEKVTLCISVLISLTFLVLTETISTSVLVPLIGEYLIFT 309  
 Qy 301 MFMVASSVYVTVVLYNHIRTADTHEMPWIKSYPLQWLPWILMRSPGKTKITRTIMMN 360  
 Db 310 MIFTLSIVTIVFVNVHRYTPHTMPSWVKTFNLNPVMTRP-----357  
 Qy 361 TRMRELELKERSSSSLLANVLDIDDDFRIGCPPNASTGNL ----- GPGCS ----- 408  
 Db 358 -----TSNEGNAQKPRPLYYGAELSNLNCFRSAESKGCKEGYP 395  
 Qy 409 -----IPTTDERRSFVRESTMEDVGG-----GLGSFHREHLILRQLFETARMKK 454  
 Db 396 QDGMCYGCYCHRRIKISNFNSANLTSRSSSESVDAILSLALSPEIKEAQSVKYTAENMKA 455  
 Qy 455 ADEAEELISDWKFAAMVDRFCFLVFTLFTIATAVLL 493  
 Db 456 QNEAKEIQDDWKYVAMVIDRFLWFTLVCLGTAGLFL 494

RESULT 8  
 ACH3 RAT STANDARD PRT; 499 AA.  
 ID ACH3 RAT  
 AC P04157;  
 AC 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DB Neuronal acetylcholine receptor protein, alpha-3 chain precursor.  
 GN CHRNA3 OR ACRA3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN NCBI\_TaxID=10116;  
 RN [1]  
 RA Heinemann N.A.  
 RA MEDLINE=86118671; PubMed=3753746;  
 RA SEQUENCE FROM N.A.  
 RA Boulter J., Goldman D.J., Martin G., Treco D.,  
 RA Heinemann S.F.,  
 RA Patrick J.,  
 RA Evans K.,  
 RA Boulter J.,  
 RA "Isolation of a cDNA clone coding for a possible neural nicotinic acetylcholine receptor alpha-subunit.",  
 RA Nature 319:358-374(1986).  
 RA [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=88041184; PubMed=244984;  
 RA Boulter J., Connolly J.G., Denoris E.S., Goldman D.J., Heinemann S.F.,  
 RA Patrick J.,

CC	DR	EMBL; X03440; CAA27170; 1-;
	DR	EMBL; L31621; AAA41673; 1-;
	DR	EMBL; AAA18001; 1-;
	InterPro; IPR06029; Neu_channel memb.	
	DR	InterPro; IPR06202; Neu_chan_LBD;
	DR	InterPro; IPR06201; Neu_channel.
	DR	Pfam; PF02931; Neu_chan_LBD; 1.
	DR	Pfam; PF02932; Neu_chan_memb; 1.
	DR	PRINTS; PRO0252; NEUROCHANNEL; 1.
	DR	TIGRFAM; TIGR00860; LIC; 1.
	PROSITE; PS00236; NEUROTRION_CHANNEL; 1.	
	DR	Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW	KW	Transmembrane; Multigene family.
FFT	SIGNAL	1 25 POTENTIAL.
FFT	CHAIN	26 499 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT	DOMAIN	26 234 ALPHA-3 CHAIN.
FT	TRANSMEM	235 259 EXTRACELLULAR.
FT	TRANSMEM	267 285
FT	TRANSMEM	301 322
FT	DOMAIN	323 471
FT	TRANSMEM	472 491
FT	DISULFID	491 167
FT	DISULFID	153 167 BY SIMILARITY.
FT	DISULFID	217 218 ASSOCIATED WITH RECEPTOR ACTIVATION
FT		(BY SIMILARITY).
CARBOHYD	CARBOHYD	49 49 N-LINED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	CARBOHYD	166 166 N-LINED (GLCNAC. . .) (PROBABLE).
SEQUENCE	SEQUENCE	499 AA; 56991 MW; D66491E832B9C34 CRC64;
3	Query Match	37.0%; Score 977.5; DB 1; Length 499;
3	Best Local Similarity	40.2%; Pred. No. 2.1e-77;
3	Matches 201;	Conservative 95; Mismatches 177; indels 27; Gaps 8;
Qy	Db	PLMLAIALALLLPVSEQGPHEKRLLMALLANYNTLRRPVANESEPLEVRFLGTLTQQLIDV 62
Qy	Db	PLSLMLVLMILPAAASASEAHRLLFQYLFEDYNEIIRPVANTSHPVVIQFETMSMQLVKV 68
Qy	Db	DEKQNQILITNLWLSLEWNDYNLRWNNSSEYGGYKDLRITPNKLWKPDLYMNSADEGFDTGCT 122
Qy	Db	DEVNQIMETNLWLKIQWDXKLKWKSDSYQGYFEMRVPAAEKIWKPDIVLYNNADGDFQVD 128
Qy	Db	YQTNVYVRSQGSCCLYPPGTFKSTCKMDIANPFDDOHDCKMKGFSWYTDGENQDLILVKKDE 182

Db	129	DKTKALLKYTGEGTVWIPPAFKSSCKIDVYTFPPFYQNCCTMKFGSWSYDKAKIDLVLIG-187
Qy	183	AGGDLSDFLTNGEWLIGMPGRNNTITYACCPPEPVWDVFITIMIRRLLYFFNLLIVPCV 242
Qy	188	SSMLKDYNESGEAAIIKAPGYKEIKYNCCEIYQDITYSLYIRRLPLFYTINIIIPCL 247
Db	243	LISSMALIGETLPPSGEKLTLGTYTLLSLTFLNVLVAETLPOVSDAIPLGLTYFNCLMFE 302
Db	248	LISFIVLVYLPSCGEKVTLCSVLISITVFLVITETIPSTLVLPIGLGEYLFTM1 307
Qy	303	MVASSVLTVVNLNTHRZADIHMPOWKSVFLQWLPIWLRMSRP--GKKITRKTKT-IMM 359
Db	308	FVTLSIVTIVFLNVHYRTPPTHMPMTWKAVFLNLLPRVMEMTRPSEGDTPTTRTFY 367
Qy	360	NTRRMRELELKERS-SKSLLANVLDDDFRHGPPPNSTASTGNLGPGCCSIFR--TDFFR 415
Db	368	GAEELSNLNCGFSRAKSCKC-----KEGYPOQDGTCGY-----CHHRVYISNSF 410
Qy	416	RSFYPKPSTMEDVGG--GLSHSHREHLHLIRELOFTARMKKKADEFELISDMKFAAMVYD 473
Db	411	ANLTRSSSSSVNAWLSSLSPRIKEATQSVKYTAENMKAQNYAKEIODDWKXVAMVYD 470
Qy	474	RFCLEVFTLFTIATAVLL 493
Db	471	RIFLWVFLVLCILGTAGFL 490
RESULT 9		
ACH3_BOVIN		
ID	Q07263;	STANDARD;
AC	Q07263;	PRY; 495 AA.
DT	01-OCT-1994 (Rel. 30, Created)	
DT	01-OCT-1994 (Rel. 30, Last sequence update)	
DT	28-FEB-2003 (Rel. 41, Last annotation update)	
DE	Neuronal acetylcholine receptor protein, alpha-3 chain precursor.	
GN	CHRNA3.	
OS	Bos taurus (Bovine).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	
OC	Bovidae; Bovinae; Bos.	
OX	NCBI_TaxID:9913;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE:92319195; PubMedId=1620271;	
RA	Criado M., Alamo L., Navarro A.;	
RT	"Primary structure of an agonist binding subunit of the nicotinic acetylcholine receptor from bovine adrenal chromaffin cells.";	
RT	Neurochem. Res. 17:281-287(1992),	
RL	-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma membrane.	
CC	- ! - SUBUNIT: Neuronal AChR seems to be composed of two different type CC of subunits: alpha and non-alpha (beta).	
CC	- ! - SUBCELLULAR LOCATION: Integral membrane protein.	
CC	- ! - SIMILARITY: Belongs to the ligand-gated ionic channel family.	
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CC	EMBL; X57032; CAA40348.1; -	
DR	PIR; S65189; S60589.	
DR	InterPro; IPR006029; Neu_channe1_memb.	
DR	InterPro; IPR006202; Neu_ chan_LBD.	
DR	InterPro; IPR006201; Neu_r-channel.	
DR	Pfam; PF02931; Neu_ chan_LBD; 1.	
DR	PFam; PF02932; Neu_r-chan_memb; 1.	
DR	PFam; PF02933; Neu_r-chan_memb; 1.	

DR TIGRFAMS; TIGR00860; LIC; 1.  
 PROTEIN; PS00336; NEUROTRANSMITTER; ION CHANNEL; Ionic channel; Glycoprotein; Signal;  
 KW Transmembrane; Multigene family.

KW SIGNAL 1 21  
 FT DOMAIN 22 495  
 FT DOMAIN 22 230  
 FT TRANSMEM 231 255  
 FT TRANSMEM 263 281  
 FT TRANSMEM 296 318  
 FT DOMAIN 319 467  
 FT TRANSMEM 468 487  
 FT DISULFID 149 163  
 FT DISULFID 213 214  
 FT CARBOHYD 45 45  
 FT CARBOHYD 162 162  
 SEQ SEQUENCE 495 AA; 56914 MW; 322825629821EA07 CRC64;

Query Match 36.8%; score 970.5; DB 1; Length 495;  
 Best Local Similarity 39.8%; Pred. No. 8 3e-77;  
 Matches 198; Conservative 93; Mismatches 181; Indels 25; Gaps 7;

QY 5 LAALALLALLPVSEQGPHEKRLLNALLNANTLERPVANESEPLEVRFLQLQOIDVDE 64  
 DB 7 LRLRLLPLLPAVASTDAEIRLFLERLFEDNEIRPVANESEPLEVRFLQLQOIDVDE 66

QY 65 KNOLLITINWISLENDYLNRWDSSEYGGYKDLRITPNKLWKPDVLMYNSADEGFDGTQ 124  
 QY 67 VNQIMETNLWALKQINNDYKLNPSDYYDGAEEFRMTPAELWKPDVLYNNAVGDFQVDDK 126

QY 125 TNVVVRSGGSLLYVPFGIFKSTCRMDIAWPFDDCHMKFGSWYDGNOLDLVLRDEAG 184  
 DB 127 TKALKYTGEVTVIPIAFKSSCKDVTYFPFDYQNCTMKFGWSYDKNLIG-SS 185

QY 185 GDLSDEFTINGEWYLGMPGKRNNTITYAACCPBPYVDTFTIMRRTLYPFNLIVPCVLI 244  
 DB 186 MNLKQDWESGWAIILKAPGYKHDIKYNCCB1YLPDTSYLRRLPLFYNLIPCLLI 245

QY 245 SSMALIGFTLPPDSGERKLTLGVTILLSLTVFLNVAETPLPQVSDA1APILGTYFNCFMFV 304  
 DB 246 SFLTVLVFYLPSDCGEKVLTCISVLISLTVFLVLTETIPSTS1VPLIGEYLLFTM1FV 305

QY 305 ASSVLTVVVLYNHTADTHMPOMKVSFLQWLPWLLMSRPK--KITRKTMINT 361  
 DB 306 TLSIVTIVFLVNHTRPTHTMPAWKTFLNLLPRVMMTRPASNEGNTQRPRPFYSA 365

QY 362 RMREELPKRSKSSLANVLDIDDDFRHGPAPPNSTAATENLPGC5IFR---TDFRSR 418

DB 366 ELSNLNCFSRLESVKC-----KEGVY----CQDGLCG-YCHHRAKISNSFANL 409

QY 419 VRPSTMEDYGG--GIGSHHRELHLILRELOFQTARMKADEEAELJSDWKFAAMYVDRFC 476

DB 410 TRSSSESVDAVLSSALSPEIKAQSIVTAENNAQNEAKEIQQDWKRYVAMVYDRFC 469

QY 477 LEFVELFTIATVAVL 493

DB 470 LWFFFLVCLTGATGFL 486

RESULT 10  
 ACH1 DRONE STANDARD; PRT; 567 AA.

ID ACH1\_DRONE; QsvC74; Campbell K.S., Matthews B.B., Campbell K.S.,  
 AC P09478; QsvC74; Mungall C.J., Matthews B.B., Campbell K.S.,  
 DT 01-MAR-1989 (Rel. 10, Created) RT; Crosby M.A., Mungall C.J., Campbell K.S.,  
 DT 10-OCT-2003 (Rel. 42, Last sequence update) RT; Crosby M.A., Mungall C.J.,  
 DT 10-OCT-2003 (Rel. 42, Last annotation update) RT; Crosby M.A., Mungall C.J.,  
 DE Acetylcholine receptor protein, alpha-like chain 1 precursor. RT; Crosby M.A., Mungall C.J.,  
 DE NAC ALPHA-96AA OR ACRB OR AIS OR ACR96AA OR CG5110. RT; Crosby M.A., Mungall C.J.,  
 OS Drosophila melanogaster (Fruit fly). CC; Crosby M.A., Mungall C.J.,  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; CC; Crosby M.A., Mungall C.J.,  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; CC; Crosby M.A., Mungall C.J.,

OC Ephydrioidea; Drosophilidae; Drosophila. OC  
 RN [1] \_TaxID=7227; RN  
 RN SEQUENCE FROM N.A. RN  
 RN STRAIN=Oregon R; RN  
 RC MEDLINE=98283626; PubMed=2840281; RN  
 RA Bossy B., Ballivet M., Spierer P.; RN  
 "Conservation of neural nicotinic acetylcholine receptors from Drosophila to vertebrate central nervous systems."; RN  
 RT Drosophila J. 7:611-618(1988). RN  
 RL EMBO J. 7:611-618(1988). RN  
 [2] RN  
 RN SEQUENCE FROM N.A. RN  
 RC STRAIN=Berkley; RN  
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D., Gocayne J.D.,  
 MEDLINE=20196006; PubMed=10731132; RN  
 RX Adams M.D., Celiker S.E., Holt R.A., Galle R.E., Galle R.E.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Hoskins R.A.,  
 RA George R.A., Lewis S.E., Richards S.E., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazquez R.G., Champé M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Asbury A.A., An H.-J., Andrews P.-Fannoch C., Baldwin E.M.,  
 RA Ballieu R.M., Basu A., Baxendale J., Bayrakaroglu L., Beasley S.,  
 RA Beezon K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Botchkova D., Botchkova D., Brockmann P., Brottier P.,  
 RA Burtsis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davies P., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Dietz I., Dietz I.,  
 RA Dondur K., Doup L.E., Downes M., Dugan-Rocha S., Dunikov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraria S., Fleischmann W.,  
 RA Fesler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Houston D., Houston K.A., Howland T.J., Wei M.-H., Ibebewam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimball B.E., Kodira C.D., Kraft C., Kravitz S., Kulpa D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milashina N.V., Morris J., Mosherfi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muany D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,  
 RA Palazzolo M., Pittman G.S., Pollard J., Puriv V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shu B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin B.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."; RT  
 RL Science 287:2185-2195 (2000). RN  
 [3] RN  
 RP REVISIONS; RT  
 RX MEDLINE=22426069; PubMed=12537572; RN  
 RA Misra S., Crosby M.A., Mungall C.J., Campbell K.S., Campbell K.S.,  
 RA Hradecy P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whittfeld E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bellenourt B.R., Celiker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review"; RT  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002). CC  
 CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma membrane. CC  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. CC  
 CC -!- TISSUE SPECIFICITY: CNS in embryos. CC  
 CC -!- DEVELOPMENTAL STAGE: Late embryonic, late pupal and second instar larvae stages. CC

CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.

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CC X07194; CAA30172.1; -.

DR EMBL; AE03747; AAFAE1.

DR PIR; S00381; ACEFA1.

DR Flybase; FBgn0000036; nacr-alpha-96Aa.

DR InterPro; IPR006029; Neu\_channel memb.

DR InterPro; IPR006202; Neu\_chan\_LBD.

DR InterPro; IPR006201; Near\_channel.

PFam; PF02931; Neu\_chan\_LBD.

PFam; PF02932; Neu\_chan\_memb; 1.

DR PRINTS; PRO0232; NRIONCHANNEL; 1.

TIGRFAMS; TIGR000860; LUC; 1.

DR PROSITE; PS002336; NEUROTR\_ION\_CHANNEL; 1.

REceptor; Possessing membrane; Ionic channel; Glycoprotein; Signal;

KW Transmembrane; Multigene family; Polymorphism.

SIGNAL 1

FT CHAIN 22

ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-

LIKE CHAIN 1.

FT DOMAIN 22 240

EXTRACELLULAR.

FT TRANSMEM 241 264

FT TRANSMEM 272 290

FT TRANSMEM 3.06 325

FT DOMAIN 3.26 513

FT TRANSMEM 5.14 532

FT DISULFID 5.14 532

FT DISULFID 149 163

FT DISULFID 222 223

ASSOCIATED WITH RECEPTOR ACTIVATION

(BY SIMILARITY).

FT CARBOHYD 45 45

N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 233 233

N-LINKED (GLCNAC. .) (POTENTIAL).

FT VARIANT 538 538

Y -> H.

FT CONFLICT 108 108 L -> H (IN REF. 1)

FT SEQUENCE 567 AA; 64019 MW; OBE1F71FB2A92AC CRC64;

Query Match Score 964.5; DB 1; Length 567;

Best Local Similarity 36.5%; Pred. No. 3.3e-160; Indels 91; Gaps 9;

Matches 199; Conservative 95; Mismatches 160;

QY 21 PHEKRLLNALLANVNTLEPVRVANESEPLEVRVFRGTLQLIDDEKNOILLTNWLSLWN 80

DB 23 PDAKRLYDOLSNVRLTIREGVGNNSDLRTYGMURLSQIDVNKLQNOMITNNWVEQWN 82

QY 81 DYNLRWNDEBGGYKDRLRTPKWKPDYLMYNSADEGFDGTQYTNVVRSGSCLYYPP 140

DB 83 DYKUKWNPPDYGGDTLHPSSEH1WLDDLVLYNNADGNVTDGQNLDSLDEFT 192

QY 141 GIPKSTCKMDIAWFPFDODHCMDMKGSTMVYDGQNLDSLDEFT 192

DB 253 TLPPDSGEKLTGVTLLSLTVFLNLVAETLPQVSDAIPLLGTYFNCMFMVASSVYLV 312

DB 143 AIVKSFCEDVVEYPFDCTCMEKSGSTMVYDGWDLRHLQTAQDSDNTEVGIDLQDYY 202

QY 193 NGEWYLMGPKNTNTYACCPEPYVDVTMIRRRLYYFVNLLIVCPLSSMALLGF 252

DB 203 SVENDIMRPAVNEKFISCCEEFYLDIVENLTKRKTLFYTNNLIIQCGISFLSVLF 262

QY 253 TLPPDSGEKLTGVTLLSLTVFLNLVAETLPQVSDAIPLLGTYFNCMFMVASSVYLV 312

DB 263 YLPDSGEKISLCSILLSTVFLLAELIPTSLTLLGKLLFTMLVLTSVWT 322

QY 313 VVJNYXHRTADIHMPONKTSVSKVFWLPIRMSRPGKIKTRKTMNTMRMLELKERS 372

DB 323 AVLAVNFERSPVTHMAPWQRLPCLICERPKCE-----EPEEQD 367

QY 373 SKSSLANVU---DID----DDFRHG-----PPPP 394

DB 368 PPEVLTQDVFHLPDPDVDFKFTNYDSSKRFSGGDYGIPALPASHRFDLAAAGGISAHCFAEPLLP 427

QY 395 NS-----TASTONLGPCC-----SIFTDFRRSFVPRSTMEDVGGGIJSHH 436

DB 428 SSLPLPGADDLFLSSGLNGDISPCCPAAAALADSLSPTEP-----

CC -!- SIMILARITY: Belongs to the acetylcholine receptor alpha-1 subunit.

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CC X07194; CAA30172.1; -.

DR EMBL; P09481; Valera S., Rungger D., Bertrand S.,

DR AC P09481; Valera S., Rungger D., Bertrand S.,

DR DT 01-MAR-1989 (Rel. 10, Created)

DR DT 01-APR-1993 (Rel. 25, Last sequence update)

DR DT 28-FEB-2003 (Rel. 41, Last annotation update)

DB DB Neuronal acetylcholine receptor protein, alpha-3 chain precursor.

OS OS Gallus gallus (Chicken)

OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC OC Gallus.

NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91039210; PubMed=16987777;

RA Courtier S., Erkman L., Valera S., Rungger D., Bertrand S.,

RA Boultter J., Ballivet M., Bertrand D.;

RA RT "Alpha 5, alpha 3, and non-alpha 3. Three clustered avian genes encoding neuronal nicotinic acetylcholine receptor-related subunits." J. Biol. Chem. 265:17560-17567(1990).

RN [2]

RP SEQUENCE OF 81-496 FROM N.A.

RX MEDLINE=88281624; PubMed=3267226;

RA Ref P., Onyeiser C., Alliod C., Couturier S., Ballivet M.;

RT "Genes expressed in the brain define three distinct neuronal nicotinic acetylcholine receptors." J. Biol. Chem. 265:17560-17567(1990).

RC TISSUE=Brain;

CC -!- FUNCTION: After binding acetylcholine, the AchR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma membrane.

CC -!- SUBUNIT: Neuronal AchR seems to be composed of two different type of subunits: alpha and non-alpha (also called beta). A functional receptor seems to consist of two alpha-chains and three non-alpha chains.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- DEVELOPMENTAL STAGE: High levels in the developing ciliary and superior cervical ganglia.

CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.

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DR EMBL; M37336; ARB48559\_1; -.

DR EMBL; X07345; CAA30284\_1; JOINED;

DR EMBL; X07346; CAA30284\_1; JOINED;

DR EMBL; X07347; CAA30284\_1; JOINED;

DR EMBL; S00378; ACC33N.

DR InterPro; IPR006029; Neu\_channel\_1 memb.

DR InterPro; IPR006020; Neu\_channel\_1BD.

DR InterPro; IPR006201; Neu\_channel\_2.

DR Pfam; PF02931; Neur\_chan\_LBD; 1.  
 DR PR02932; Neur\_chan\_memb; 1.  
 DR PRNTMS; PR00232; NPIONCHANNEL.  
 DR TIGR4MS; TIGR00860; LIC; 1.  
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.  
 KW Postsynaptic membrane; Ionic CHANNEL; Glycoprotein; Signal;  
 KW Transmembrane; Multigene family.  
 SIGNAL 1 22  
 FT CHAIN 23 496 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,  
 ALPHA-3 CHAIN.  
 FT DOMAIN 23 231 EXTRACELLULAR.  
 FT TRANSMEM 232 256  
 FT TRANSMEM 264 282  
 FT TRANSMEM 298 319  
 FT DOMAIN 320 468 CYTOPLASMIC.  
 FT TRANSMEM 469 488 BY SIMILARITY.  
 FT DISULFID 150 164 ASSOCIATED WITH RECEPTOR ACTIVATION  
 (BY SIMILARITY).  
 FT DISULFID 214 215 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (PROBABLE).  
 FT CARBOHYD 163 163 SEQUENCE 496 AA; 57027 MW; FD5BC02A9B601FE CRC64;  
 SEQ 7 ALALLALLPVSEQQ--PHEKRLLNALLANNTLRLPVANESEPLEVRFLQLQI DY 62  
 6 ALLLTAVCILFQGCGGSEPERLYALAKFKNYQNFQTPVKNAQDFQVMSQLVKV 65  
 QY 63 DEKQNQLLITINWISLSPWDNYLNLRSDEYGGVKKDLRITPNPKLWKEDVLMNSADGFDT 122  
 DB 66 DEVNQIMETINWIKLHTWNDYKLRLRNPDYGAEEFRVPKGQJWKPDKLVLVNNAVCFD QVD 125  
 QY 123 YQTNVVVRSGSCLYPGIFKSTKNDIANFPDFDQHCDMKFGSMTYDNQDLIVLKE 182  
 DB 126 DKTALKLKYTGDTWIPPAFKSSCKDVIQYFPFDYQNCTMKFGWSYDZAKIDLVLIGS 185  
 QY 183 AGGDLSPFTINGEWYLGMGPCKNTTYYACCEPEPYDVTFTIMIRRTLYFFNLLVPCV 242  
 DB 186 T-MNUKDYSWEWAIIKAPGYKHDXNCCBEITDITYSLVYRPLPTINMLPCL 244  
 QY 243 LISSMALLGIFTLIPDSGEKLTGVTLLISLTIVLNIAETLPQVSDAIPLLGTYENCIMF 302  
 DB 245 LLSFLTLYVFLPSDCCEKYLICLISVLISLTIVLLVTECPLSTSLLVPLIGEYLFTMI 304  
 QY 303 MVAASSVLLTVVVLNHYRTADLHEMPQWIKSVFLQWLPWLRMSRGKTRKTIMNTR 362  
 DB 305 FVTLSITIVTVFLVHYRTPKTHMPWVWRTRTFLNLPPLPRIMFMTRP----- 350  
 QY 363 MRELEKXERSKSLLANVLDDDFRIGPPPNSTATGNG----- 404  
 DB 351 -----TSDEENNQKPKPFYTSFESNINCFNSSEIKCKDGTVQCD 390  
 QY 405 PGCSIFR-----TDFRSFYRPSMTEDVGG--GLGSHHRELHLIRELQFITARMKAD 456  
 DB 391 MACSCCCYQRMKFSDFSGNLTSSSESDVLFSPMRDATESVYIAENNMQDN 450  
 QY 457 EAELISDWKAAMTVDRFCFLVFUTLITATVAVL 493  
 DB 451 EAKEIQDDWKVYAMVIDRFLWFVILGTAGFL 487

OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).  
 OC Lukaryote; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingidae;  
 OC Sphingidae; Sphinginae; Manduca.  
 RN [1].  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98424077; PubMed=975155;  
 RA Eastham H.M.; Lind R.J.; Eastlake J.L.; Clarke B.S.; Towner P.,  
 RA Reynolds S.E.; Wolstenholme A.J.; Wonnacott S.;  
 RT "Characterization of a nicotinic acetylcholine receptor from the  
 insect Manduca sexta."  
 RL Eur. J. Neurosci. 10:879-889(1998).  
 CC -|- FUNCTION: After binding acetylcholine, the AChR responds by an  
 CC extensive change in conformation that affects all subunits and  
 CC leads to opening of an ion-conducting channel across the plasma  
 CC membrane (By similarity).  
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -|- SIMILARITY: Belongs to the ligand-gated ionic channel family.  
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 CC or send an email to license@isb-sib.ch).  
 CC  
 DR EMBL; Y09795; CAA70928; 1.  
 DR InterPro; IPR006029; Neu channel memb.  
 DR InterPro; IPR006202; Neu chan LBD.  
 DR InterPro; IPR006201; Neu chan channel.  
 DR Pfam; PF02931; Neu chan LBD; 1.  
 DR Pfam; PF02932; Neu chan memb; 1.  
 DR PRINTS; PRO0025; NRIONCHANNEL.  
 DR TIGRFAMS; TIGR00860; LIC; 1.  
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.  
 KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;  
 KW Transmembrane; Multigene family.  
 FT SIGNAL 1 21  
 FT CHAIN 22 516  
 FT DOMAIN 22 243  
 FT TRANSMEM 244 264  
 FT TRANSMEM 274 294  
 FT DOMAIN 306 326  
 FT TRANSMEM 327 465  
 FT TRANSMEM 466 486  
 FT DISULFID 149 163  
 FT DISULFID 222 223  
 FT CARBOHYD 45 45  
 FT CARBOHYD 132 132  
 FT CARBOHYD 233 233  
 SQ SEQUENCE 516 AA; 58720 MW; E7A71E8C45D13B2 CRC64;  
 Query Match 35.9%; Score 946.5; DB 1; Length 516;  
 Best Local Similarity 39.7%; Pred. No. 1.1e-4;  
 Matches 195; Conservative 84; Mismatches 171; Indels 41; Gaps 6;

QY 21 PHEKRLLNALLANTLRLPVANESEPLEVRFLQLQI DY 62  
 DB 23 PDAKRLYDDLSNNVNNKLVRPVNLNSDALTRIKLKSQOLIDVNQNQIMTNLWVQSWY 82  
 QY 81 DYNLRWNDSSEYGGKDLRITPVANESEPLEVRFLQLQI DY 62  
 DB 83 DYKLSPSEPRETGGVNLHVPDHNWVADGNFETVLAQATLNNTGRVWRPP 140  
 DB 83 DYKLSPSEPRETGGVNLHVPDHNWVADGNFETVLAQATLNNTGRVWRPP 142  
 DB 141 GIKF87CKMDTAWFEPDDOHDMDKFGSMWTDGNOI.DLVLKDEAGG-----DLSDFIT 192  
 DB 83 ID 91766; STANDARD; PRT; 516 AA.  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Acetylcholine receptor protein, alpha-like chain precursor (MARAL).  
 QY 193 NGEWYLIGMPGKKTNTITYACCPEPYDVFTIMIRRRLYYFFNLLIVPCVLISMALLGF 252  
 QY 93 NGEWYLIGMPGKKTNTITYACCPEPYDVFTIMIRRRLYYFFNLLIVPCVLISMALLGF 252

RESULT 12  
 PCH1\_MANSE ID ACH1\_MANSE  
 AC P91766;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Acetylcholine receptor protein, alpha-like chain precursor (MARAL).  
 QY 93 NGEWYLIGMPGKKTNTITYACCPEPYDVFTIMIRRRLYYFFNLLIVPCVLISMALLGF 252

Db	203	SVENDILEPPAVNSNEKFYTCCTCDBEYLDTENITMRRKTYFYTNYNLLIPCMGIFSLTVLVP	262		FT	CHAIN	24	557	ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1 CHAIN.
Qy	253	TLPEDSGEKLTVLLGTIVTLLVTPVDAILEFLGTYFNCTIMFMVASSVLTIV	312		FT	DOMAIN	24	244	EXTRACELLULAR.
Db	263	YLPDSGKEVKVSLTISILLSTUTFILLAKIIPPTSLVVFILGFKEVLTFMIDDFSICV	322		FT	TRANSMEM	245	266	
Qy	313	VVNVYHARATDADHEPONTKSVFLQWLPILRMSRPGKKI--TRKTIMMNTRMRELELK	369		FT	TRANSMEM	274	294	CYTOSMATIC.
Db	323	VVNVHFRPQRQTHMSPWVRVFHVLPPLVMRPHRLDPHRSRAGLVTAEGERTLW	382		FT	TRANSMEM	308	329	
Qy	370	ERSSKSLLANVLDIDDDFHGPPPNNSTASTGNLGP--GCSIERTDFRRSFVRPSTMEDV	427		FT	DISULFID	501	523	BY SIMILARITY.
Db	383	DEGSPPGV-----PAPRPPCPAPLAACAA-----PAEAPAL 416			FT	DISULFID	151	165	ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
Qy	428	GGGGSHHR--ELHLLRLQLQTARMKKADEFELISTWKPEAMMVVDFECLFVFTDFTI	485		FT	CARBOHYD	47	47	N-LINKED (GLCNAC. .) (POTENTIAL).
Db	417	CDALARWRHCPCEHLKAIDSYNTAQDTRKEESTRVKEDWKYVAMVLDRLPFLWIFTLAVV	476		FT	CARBOHYD	235	235	N-LINKED (GLCNAC. .) (POTENTIAL).
Qy	486	IATVAVLISAP 496			FT	DOMAIN	382	400	ALPHA-SER-RICH.
Db	477	VGSAGIILOAP 487			FT	DOMAIN	406	422	HIS-RICH.
Qy					SQ	SEQUENCE	557 AA;	63026 MW;	168389887DFDF3E CRC64;
									Query Match 35.8%; Score 944; DB 1; Length 557;
									Best Local Similarity 36.9%; Prod. No. 2e-74; Mismatches 181; Indels 66; Gaps 7;
									Matches 201; Conservative 96; MisMatches 181; Indels 66; Gaps 7;
					Qy	1	MAPMLAIALALLLPVSSEOGPHERKLNLALLANNTLERPVANESEPLEVRFGTLQQII	60	
					Db	65	DLMRQDQLLTINWLEHHWQDHFRWFDAYEGVTELYVPSBTETWLWDIVLYNAQDRYV	120	
					Qy	5	LPPMLLMLLMLLHPAANPDAKRFLYDDLSNWNRLPVSNTNTDVLVKUGLRLSQLI	64	
					Db	61	DYDEKNCQLLITNTIWLSSLWNDYNLRWNDSEYGGYKDLRTPNKLWKPDPYLMNSADEGFD	120	
					Qy	121	GTYQTQVVYVRSGGSCLYYPGPIRKSTCKMDIAFMFPDDQHCDMKFGSMTYDGQNQLDLV-	178	
					Db	125	VTTMKAVALHHTQSKVWWTPAIIKSCKSCEDVRLFPDQTCMFKGSMTYDGQDQIDLKH1	184	
					Qy	179	----LKDDEAGDPLSDFITNGWYLIGMPGRNTYACCPBVDYFTIMIRRTLY	232	
					Db	185	NQKYDDNKVKGIDLREYYPSEWDLGVPAAEHKEYKYPCCAEPYDFFNITLRKTLF	244	
					Qy	233	YFFMLIYPCVLISSMALIIGFTLPPDSEGEKLTVLGTIVTLLSLTVPLNLYAETLPOVSDATPL	292	
					Db	245	YTNVLIVCGVSYLSVIVLPADSGKIALCISLISQTMFLLSSBIIPTSLALPL	304	
					Qy	293	LGTYFCNCFMVMASVSVLTVLNVHRTADHMPOMIKSYPLQWLPWILMRSRPGK-	350	
					Db	305	LGKYLFLFTMVGLSVVITMVNVHKVKEPKSTHKMAPAVKRYEIRLPKLLMRPEQLI	364	
					Qy	351	-KTRTRKTMNMTRMRELELKERSKSLIA--NVLDIDDDFRH---	389	
					Db	365	ADLASKRLLRHAINSKLSAAA:AAA:AAA:AAA:AAA:AAA:AAA:AAA:AAA:	424	
					Qy	390	GPPPNST-ASTGNLGPCCSISPRTDFRRSFVRPSTMEDVGGGLS-----	433	
					Db	425	RPGGNGLHSATNRFGSAGAF-----GGPSVVGLDGSLSDVATRK	466	
					Qy	434	-HHRELHLILRELQFTTARMKKADEFELISDWKFAAMVYDRCFLYETLFTLTIAVTAVL	492	
					Db	467	KYFELERKAHNVLFIQNHMQRODEFDAEDQDWGFVAMVLDRFLWIFTIASIVGTEAIL	526	
					Qy	493	LSAP 496		
					Db	527	CEAP 530		
									RESULT 14
									ACH2_DROME
									AC P17644; Q9VC73;
									ID 1-AUG-1990 (Rel. 15, Created)
									DT 01-AUG-1990 (Rel. 15, Last sequence update)
									DT 10-OCT-2003 (Rel. 42, Last annotation update)
									DE Acetylcholine receptor protein, alpha-like chain 2 precursor.
									GN NACR-ALPHA-16AB OR ACRE OR SAD OR ACR96AB OR CG6844.
									OS Drosophila melanogaster (Fruit fly).
									OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
									CC SIGNAL 1 POTENTIAL.

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CC PIR: X55439; CAA9081.1; -

CC InterPro: IP006039; Neu channel memb.

CC InterPro: IP006202; Neu<sup>+</sup> chan LBD.

CC InterPro: IP006211; Neu<sup>+</sup> channel.

CC PFam: PF02931; Neu<sup>+</sup> chan\_LBD; 1.

CC PFam: PF02932; Neu<sup>+</sup> chan\_memb; 1.

CC PRINTS: PR0052; MRIONCHANNEL.

CC TIGRFAMS: TIGR00850; LIC: 1.

CC PROSITE: PS00236; NEUROTR\_ION CHANNEL, 1.

CC Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;

CC Transmembrane; Multigene family.

CC SIGNAL 1 POTENTIAL.

OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	Stapleton M., Carlson J.W., Brokstein P., Yu C., Champé M., George R.A., Guarin H., Krommiller B., Paclib J.M., Park S., Wan K.H., Rubin G.M., Celinker S.E., "A Drosophila full-length cDNA resource." ;
NCBI_TAXID=[1]	Ephydriidae; Drosophilidae; Drosophila.	RT "A Drosophila full-length cDNA resource." ;
RN	SEQUENCE FROM N.A.	RL Genome Biol. 3 :RESPARCH080_1-RESPARCH080_8 (2002).
RC	TISSUE=Head;	CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma membrane
RX	MEDLINE=90301489; PubMed=2114015;	CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
RA	Baumann A., Jonas P., Gundelfinger E.D., "Sequence of D alpha 2, a novel alpha-like subunit of Drosophila nicotinic acetylcholine receptors.", Nucleic Acids Res. 18:3640-3640(1990).	CC -!- TISSUE SPECIFICITY: CNS in embryos.
RL	[2]	CC -!- DEVELOPMENTAL STAGE: Late embryonic and late pupal stages.
RN	SEQUENCE FROM N.A.	CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
RC	TISSUE=Head;	CC -!- CC
RX	SEQUENCE FROM N.A.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
RA	MEDLINE=90353591; PubMed=2117557;	CC -!- CC
RA	Jonas P., Baumann A., Merz B., Gundelfinger E.D., "Structure and developmental expression of the D alpha 2 gene encoding a novel nicotinic acetylcholine receptor protein of Drosophila melanogaster.", FEBS Lett. 269:264-268(1990).	CC -!- CC
RN	SEQUENCE FROM N.A.	CC -!- CC
RC	SEQUENCE FROM N.A.	CC -!- CC
RX	SEQUENCE FROM N.A.	CC -!- CC
RA	Sawruk E., Schloss P., Betz H., Schmitt B.; "Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD, a novel developmentally regulated alpha-subunit.", EMBO J. 9:2671-2677(1990).	CC -!- CC
RN	SEQUENCE FROM N.A.	CC -!- CC
RC	SEQUENCE FROM N.A.	CC -!- CC
RX	SEQUENCE FROM N.A.	CC -!- CC
RA	STRAIN=Berkeley;	CC -!- CC
RX	MEDLINE=20196006; PubMed=10731132;	CC -!- CC
RA	Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Branden R.C., Rogers Y.H.C., Blazej R.G., Chen L.X., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballwile R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borikova D., Botchan M.R., Bouck J., Brokstein P., Brotoier P., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., May A.D., Dew I.J., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Fostier C., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Honick J., Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibebewam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel C.E., Kodira C.D., Kraft C., Kulk D., Lai Z., Lasho P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Mertlukov G., Milashina N.V., Mobarry C., Morris J., Mosherfet A., Mount S.M., Moy M., Murphy B., Murphy L., Muzyz D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Sigen-Klamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svarskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhang X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Venter J.C.; "The genome sequence of Drosophila melanogaster.", Science 287:2185-2195(2000).	CC -!- CC
RX	SEQUENCE FROM N.A.	CC -!- CC
RA	[5]	CC -!- CC
RX	SEQUENCE FROM N.A.	CC -!- CC
RC	SEQUENCE FROM N.A.	CC -!- CC
RX	SEQUENCE FROM N.A.	CC -!- CC

Db	205 KNDKDKVKVEIGIDLRREYPPSVEIDLGVPAERHXYPPCCAEPYBDDIFFNITLRRKTLFY	264	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallius D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
Qy	234 FENLIVPCUJSSMALLGFTLPPDSEKUTLGUTILLSTYFLNVAEFLPQVSDAIPLL 293		-- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma membrane.
Db	265 TVNLIPCPVGYSVSLVFLYLPADGEKEKALCISILSQCMEFLISELIPSTSALPL 324		-- SIMILARITY: Belongs to the ligand-gated ionic channel family.
Qy	294 GTYFNCIMFWNFVASSVYLTVLTVLNTHRTADTHEPMQWIKSVFLOWLWPWLLRMSRGKKT 353		-- FUNCTION: It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/">http://www.isb-sib.ch/</a> or send an email to license@isb-sib.ch).
Db	325 GKYLLEFTMLVGLSVITLILNTHRKPSTHKPKWIRPFIREPKLPLKLMRP----- 379		--
Qy	345 RKTIMNTMRRELELKERSKSLLANVLDIDDDFRHRGPPEPNS-TASTGNLGP-GCS-LF 410		--
Db	380 -KDLRLDAAKINKVGLKFSKXTKPFQALMDQMNSGGSSPDSSLRMRMQGRVAGCCNGNH 438		--
Qy	411 RTDFRSFVRFSTMDVGCGIGS-----WHEELHLIFL 444		--
Db	439 VTTATNRF--SGLYGALGGGTSLSGYNGLPSVLSDVAAKXYPFELEKATHN 496		--
Qy	445 LQFITARMKKADEEEELISLDWKFAAMVNRDFCLFYFTLFLTIATAVLISAPHI 498		--
Db	497 VMFIOHQMFQDQEWAEDQWGFYAMMVLRFWEMFMSLVLGVFVILEGEAPSL 550		--
<b>RESULT 15</b>			
AC	ACH6_HUMAN	STANDARD;	PRT; 494 AA.
ID	Q15625;		
AC	Q15625;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Neuronal acetylcholine receptor protein, alpha-6 chain precursor.		
GN	CHRNA6		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo; OX		
NCBI_TaxID	9606;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RC	TISSUE=Substantia nigra;		
RX	MEDLINE=97062879; PubMed=8906617;		
RA	Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A., Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M., "Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits," J. Mol. Neurosci. 7:217-228 (1996).		
RA	[2]		
RN	SEQUENCE FROM N.A.		
RA	Groot Kormelink P.J.; Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.		
RA	[3]		
RP	SEQUENCE FROM N.A.		
RA	Ebihara M., Ohba H., Yoshikawa T.; "Alu and other elements in the promoter of human nAChR A6 gene (CHRNA6), direct transcriptional repression;" Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.		
RA	[4]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Skin;		
RX	MEDLINE=22388257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shanmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hipskind R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Matrusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein N.M., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rata S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullally S.J., Bosack S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muniz D.M., Soderoren E.J., Lu X., Gibbs R.A., Fahey J., Heitton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Best Local Similarity 40.2%; Score 933; DB 1; Length 494; Matches 195; Conservative 40.2%; Pred. No. 1.6e-73; Gaps 9;		
Qy	23 EKRLNALLANTNYLTERPANESEPELYRFLQLQIDVDEKNOLITNIWLSLEWNDY 82		
RA	34 EERLFHKLFSHYNQFIREPVENVSDPVTVFEEVATQLANVDEVNQIMETNLWLRHWN 93		

QY                    B3    NLRYNDSEYGGVKDLRITPNKLWPKDVLMYNSADEGFDGTQINVVRSGGSCLYVPGT 142  
 Db                    94    KLRNDPEMETYDQIETLVRPAKIKWEDIVLNAVGDFQVEGKTRALLKNGMTIWTPAI 153  
 QY                    143    FKSTCKMDIAMWFEDQHCDMKFGSSWTYDGNCNQLDLVLDKEAGG--DLSDFTINGEWYLIG 200  
 Db                    154    FKSSCEPMIDTFEPEDHQNCUSLKFGSWTYDCAEIDLII--IGSKYDMDNEWEIID 210  
 QY                    201    MPGRKNTITYACCPYVDDVFTIMIRRLYFFNLIVPCVLSSMALIGFTPPDSGE 260  
 Db                    211    ASGYXHDIKYNCCCEEYTDTITYSFYRRLMPFTYINLICOLFSFLTVFVFLPSDCGE 270  
 QY                    261    KLTLGVYILLSLSTVFLNVAETLPQVDAIPLLGTYFNCLMEMYASVLTVVVLYNHR 320  
 Db                    271    KVTLCLSVLLSLTLLVLTETIPSTSLLVPLGVYLMIFVTLSVVTVFLNTHYR 330  
 QY                    321    TADIHEMPONIKSVFELQWLFWILRNNSRPGKKITRKUTIMMNTRMRELELKERSKSLLANV 380  
 Db                    331    TPTTATMPRAVKTFLKLPLQVLLMRWPLDK-TRCT--GSDAVRGARRPAKGKLAS- 385  
 QY                    381    LDIDDDFRHGP-----PNTASTGNLGPGCSIRTDFFRSFVRPS--TMEDVVG 428  
 Db                    386    -----HGEPRLHLKECFCFHCKSNELA-----TSKERLHSQPLQWVEN-- 422  
 QY                    429    GGLGSSSHREGHLLIREQFTARMKKADEEEAEELISDWKFAMVVDRFCLEVFTLOFTIAT 488  
 Db                    423    ---SEHSPVEDVINSQFIAENMKSHNETKEVEDDWKYVAMVDRFLWVPIIVCVFGT 479  
 QY                    489    VAVLL 493  
 Db                    480    AGLFL 484

Search completed: May 7, 2004, 11:36:33  
 Job time : 10.3565 secs

Result No.	Score	Query	Match	Length	DB ID	Description
1	100.0	Q9ZI4 heliothis v	Q9ZI4	100	5	Q9ZI4 heliothis v
2	83.1	Q8T7S1 drosophila	Q8T7S1	494	5	Q8T7S1 drosophila
3	82.6	Q8T7S2 drosophila	Q8T7S2	494	5	Q8T7S2 drosophila
4	82.5	Q8T7S3 drosophila	Q8T7S3	494	5	Q8T7S3 drosophila
5	82.5	Q86MN8 drosophila	Q86MN8	494	5	Q86MN8 drosophila
6	82.4	Q8T7S0 drosophila	Q8T7S0	509	5	Q8T7S0 drosophila
7	81.7	Q8T7R9 drosophila	Q8T7R9	523	5	Q8T7R9 drosophila
8	69.4	Q9V7J9 drosophila	Q9V7J9	554	5	Q9V7J9 drosophila
9	68.3	Q9XZI3 heliothis v	Q9XZI3	496	5	Q9XZI3 heliothis v
10	68.2	Q86MM7 drosophila	Q86MM7	542	5	Q86MM7 drosophila
11	68.2	Q8T7V5 drosophila	Q8T7V5	807	5	Q8T7V5 drosophila
12	67.7	Q9WV19 drosophila	Q9WV19	545	5	Q9WV19 drosophila
13	64.6	Q8IPE2 drosophila	Q8IPE2	525	5	Q8IPE2 drosophila
14	47.7	Q9JHD6 mus musculus	Q9JHD6	502	11	Q9JHD6 mus musculus
15	47.5	Q86GA2 macaca mulatta	Q86GA2	502	6	Q86GA2 macaca mulatta
16	47.2	Q7T2U1 fugu rubripinnis	Q7T2U1	555	13	Q7T2U1 fugu rubripinnis

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OM protein - protein search, using sw model

Run on: May 7, 2004, 11:30:03 ; Search time 31.472 Seconds

(Without alignment);  
5022.709 Million cell updates/sec

Title: US-09-103-232-6  
Gapext: 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL 25:\*

1: sp\_archea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rabbit:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriaph:\*

17: sp\_archeap:\*

#### ALIGNMENTS

#### RESULT 1

ID	Q9XZI4	PRELIMINARY;	PRT;	501 AA.
AC	Q9XZI4;			
DT	01-NOV-1999 (TREMBLref).	12, Created)		
DT	01-NOV-1999 (TREMBLref).	12, Last sequence update)		
DT	01-JUN-2003 (TREMBLref).	24, Last annotation update)		
DE	Putative nicotinic acetylcholine receptor alpha subunits.			
OS	Heliothis virescens (Noctuid moth) (Owllet moth).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Diptera; Noctuoidea; Noctuidae; Heliothinae; Heliothis.			
OX	NCBI_TAXID:7102;			

RN [1] RN SEQUENCE FROM N.A.  
RA schulte T., Oellers N., Adamczewski M.;  
RT Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha subunits.";  
RL Submitted (APR-1999) to the EMBL/GenBank/DDJB databases.  
CC !- SUBCELLULAR LOCATION: INTERNAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC !- SIMILARITY: BELONGS "TO THE LIGAND-GATED ION CHANNEL FAMILY".  
DR EMBL: AF143847; AAD23698; 1. -  
DR GO; GO-0016021; C:integral to membrane; IEA.  
DR GO; GO-0005230; F:extracellular ligand-gated ion channel acti. . . ; IEA.  
DR GO; GO-0005216; F:ion channel activity; IEA.  
DR GO; GO-0030594; F:neurotransmitter receptor activity; IEA.  
DR Pfam: PF02931; Neu Chan\_LBD; 1.  
DR Pfam: PF02932; Neu Chan memb; 1.  
DR PRINTS; PP02525; NRONCHANNEL.  
DR TIGFRANS; TIGR00860; LIC; 1.  
DR PROSITE; PS00226; NEURON ION CHANNEL; 1.  
DR Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Transmembrane.  
KW KW KW KW

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

8

Result No.

Score

Query

Match

Length

DB ID

Description

SQ	SEQUENCE	501 AA;	56704 MN;	43CB0DC3960C78AB CRC64;	
	Query Match	100.0% ; Score 2640; DB 5; Length 501;			DR GO:GO:0005216; P:ion channel activity; IEA.
	Best Local Similarity	100.0% ; Pred. No. 6.9e-242;			DR GO:GO:0006811; P:neurotransmitter receptor activity; IEA.
	Matches 501; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;				DR GO:GO:0007268; P:synaptic transmission; IEA.
Qy	1 MAPMLAAALLALLPVSQGPHEKRLLNALLANTLTERVANESEPELVRFGITLQQII 60				DR InterPro; IPRO06201; Neur_chan_LBD.
Db	1 MAPMLAAALLALLPVSQGPHEKRLLNALLANTLTERVANESEPELVRFGITLQQII 60				DR InterPro; IPRO06202; Neu_channel_memb.
Qy	61 DVDEDEKQLITNIWLSLEWDYDNLWNSDSEGGYKQDLRTPNKLWKPDMYNSADEGFD 120				PFam: PF02931; Neu chan LBD; 1.
Db	61 DVDEDEKQLITNIWLSLEWDYDNLWNSDSEGGYKQDLRTPNKLWKPDMYNSADEGFD 120				DR PF02932; Neu Chan memb; 1.
Qy	121 GTYQTMNVNWSGGSCSLVPPCLFVKSTCKMDIAWFDDQHCDMKEGSMTYDGNQDLWIK 180				DR PRINTS; PRO0252; NRIONCHANNEL.
Db	121 GTYQTMNVNWSGGSCSLVPPCLFVKSTCKMDIAWFDDQHCDMKEGSMTYDGNQDLWIK 180				DR TIGR00860; LIC: 1.
Qy	181 DEAGGDLSDFTTNGEMYLIMPGRKNTITYACCPYYDVTFPTMIRRRLYYFPNLIVP 240				DR PROSITE; PS00236; NEUROR ION CHANNEL; 1.
Db	181 DEAGGDLSDFTTNGEMYLIMPGRKNTITYACCPYYDVTFPTMIRRRLYYFPNLIVP 240				KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; KW Transmembrane.
Qy	241 CVLISSMALIAGFTLPDGSGEKLTGYTILSLSLTVFLNLVAETLPQSYDAAPLLGTYFNCI 300				SQ SEQUENCE 494 AA; 56113 MW; 48127537229573FF CRC64;
Db	241 CVLISSMALIAGFTLPDGSGEKLTGYTILSLSLTVFLNLVAETLPQSYDAAPLLGTYFNCI 300				Query Match Score 2194; DB 5; Length 494;
Qy	301 MEMVASSVVLTVLWVLYNHHTADHEMPQWIKSVFLWILRNSRPGKIKTRKTMVN 360				Best Local Similarity 82.6%; Pred. No. 1.7e-199;
Db	301 MEMVASSVVLTVLWVLYNHHTADHEMPQWIKSVFLWILRNSRPGKIKTRKTMVN 360				Matches 418; Conservative 31; Mismatches 37; Indels 20; Gaps 3;
Qy	361 TRMRELELKERSKSLLANVLDIDDFRHGDPPPNSTASTCGNIGQCCSIRPTDFRSFVR 420				QY 2 APMALAL-----LALIPVSEOGPHEKRLLNALLANTLTERPVANESEPELVEYRFGLT 55
Db	361 TRMRELELKERSKSLLANVLDIDDFRHGDPPPNSTASTCGNIGQCCSIRPTDFRSFVR 420				3 SPLASLSEVLVLFIAITKESCCOPHEKRLLNLLSTINTLTERPVANESEPELVEYRFGLT 62
Qy	421 PSTMEDVGGGLGSHHRHLHLLRELOFTARMKKADEEALISDMWKFAAMVDRFCLVF 480				QY 56 LQQIDVDEKEQNQLLITNIWLSLEWDYDNLVRWNEQTYGGVQDLRTPNKLWKPDMYNSA 115
Db	421 PSTMEDVGGGLGSHHRHLHLLRELOFTARMKKADEEALISDMWKFAAMVDRFCLVF 480				63 LQQIDVDEKEQNQLLITNLWNSLLEWDYDNLVRWNEQTYGGVQDLRTPNKLWKPDMYNSA 122
Qy	481 TLFTTIAATAVLLSAPHIIVQ 501				Db 116 DEFGDGTQYQNPVVRSGGSCLYVPPGI FKSTCKMDIAWFDDQHCDMKEGSMTYDGNQI 175
Db	481 TLFTTIAATAVLLSAPHIIVQ 501				Db 123 DEFGDGTQYHNTNIVKHSGSCLYVPPGI FKSTCKMDITWFEDQHCEMKGFSWTYDGNQI 182
Qy					QY 176 DLVLDKEAGGDLSDFTTNGEWYLIGMPGRKNTITYACCPYYDVTFPTMIRRRLYYFF 235
Db					Db 183 DLVANSEDGGDLSDFTTNGEWYLIGMPGRKNTITYACCPYYDVTFPTMIRRRLYYFF 242
Qy					QY 236 NLIVPCYLISSMALLGFTLPDGSGERKLIGFTLGVYTLLSITVNLVAETLPQSYDAAPLLGT 295
Db					Db 243 NLIVPCYLISSMALLGFTLPDGSGERKLIGFTLGVYTLLSITVNLVAETLPQSYDAAPLLGT 302
Qy					QY 296 YFNICIMFMVASSVVLTVLWVLYNHHTADHEMPQWIKSVFLWILRNSRPGKIKTRK 355
Db					Db 303 YFNICIMFMVASSVVLTVLWVLYNHHTADHEMPQWIKSVFLWILRNSRPGKIKTRK 362
Qy					QY 356 TIMMNTRMRELELKERSKSLLANVLDIDDFRHGDPPPNSTASTCGNIGQCCSIRPTDFRSFVR 415
Db					Db 363 TILLSNRMKELELKERSKSLLANVLDIDDFRHGDPPPNSTASTCGNIGQCCSIRPTDFRSFVR 408
Qy					QY 416 RSFVRPSTMEDVGGGLGSHHRHLHLLRELOFTARMKKADEEALISDMWKFAAMVDRF 475
Db					Db 409 ASFGRPPTVEHHATAGCNHNKDHLTLRELOFTARMKKADEEALISDMWKFAAMVDRF 468
Qy					DE III.
Db					OS Drosophila melanogaster (Fruit fly).
CC					CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydrioides; Drosophilidae; Drosophila.
CC					CX NCBI_TaxID:7227;
RN					RN SEQUENCE FROM N_A. PubMed=1197307;
RP					RP Q8T7S2 ID Q8T7S2 PRELIMINARY; PRT; 494 AA.
AC					AC Q8T7S2; DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT	01-JUN-2002 (T-EMBLrel. 21, Last sequence update)			DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)	
DT	01-JUN-2002 (T-EMBLrel. 21, Last annotation update)			DT Nicotinic acetylcholine receptor Dalphax subunit variant type II.	
DE	Nicotinic acetylcholine receptor Dalphax subunit variant type II.			DE NACR-ALPHA_3D OR NACRALPHA_3D OR BCDDNA:GH01410 OR CG4128.	
DE	Drosophila melanogaster (Fruit fly).			OS Drosophila melanogaster (Fruit fly).	
GN	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydrioides; Drosophilidae; Drosophila.			OC	
GN				OC Hydrodiidae; Dirosophilidae; Drosophila.	
OS				OX NCBI_TaxID=7227;	
OS				RN SEQUENCE FROM N_A.	
CC				RP	



QY	416	RSFVRPSTMEDVGGGLSHREHLILRELQFTARMKKADEAELISDWKFAAMVDRF	475	Db	303	YFNCLIMFMVASSVVLTVVVLNYHRTADIHMPMIKSYFLQWLPWILMGRPRRKITRK	362
Db	409	ASFGPPTVBEHTAIGCNFRDLHJLKLQFITARMKADEAELIGDWKFAAMVDRF	468	QY	356	TIMMNTRMPELELKERSSSKSLLANVLDDDDFREGPPPNSTASTGNLGPGCSTFRTDFR	415
QY	476	CLIVFTLFTIATAVLSSAPHIVQ	501	Db	363	TILSNRMELELKERSSSKSLLANVLDDDFRHT-----TISGSGTATGSS	408
Db	469	CLIVFTLFTIATVVLSSAPHIVQ	494	QY	416	RSFVRPSTMEDVGGGLSHREHLILRELQFTARMKKADEAELISDWKFAAMVDRF	475
				Db	409	ASFGPPTVBEHTAIGCNFRDLHJLKLQFITARMKADEAELIGDWKFAAMVDRF	468
<b>RESULT 5</b>							
Q85KNB		PRELIMINARY;		PRT;	494	AA.	
ID	Q85KNB;						
AC							
DT	01-JUN-2003	(TREMBrel.	24, Created)				
DT	01-JUN-2003	(TREMBrel.	24, Last sequence update)				
DT	01-OCT-2003	(TREMBrel.	25, Last annotation update)				
DE	Nicotinic acetylcholine receptor subunit Dalphas precursor.						
GN	NACRALPHA30D.						
OS	Drosophila melanogaster (Fruit fly).						
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.						
NCBI_TaxID	4627;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RA	Millar N.S.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.						
DR	EMBL; AJ554209;						
DR	GO; GO:0016020;	C:membrane; IEA.					
DR	GO; GO:0005230;	F:extracellular ligand-gated ion channel acti.	..	; IEA.			
DR	GO; GO:0006811;	F:neurotransmitter receptor activity; IEA.					
DR	InterPro; IPR006201;	Neur_channel.					
DR	InterPro; IPR006202;	Neur_chan_LBD.					
DR	InterPro; IPR006029;	Neu_Channel memb.					
DR	Pfam; PF02931;	Neur_chan_LBD;	1,				
DR	Pfam; PF02932;	Neur_chan memb;	1,				
DR	PRINTS; PRO0252;	NPIONCHANNEL.					
DR	TIGRFAMS; TIGR000860;	LIC;	1,				
DR	PROSITE; PS00236;	NEUROTRANSMITTER_CHANNEL;	1.				
KW	SIGNAL; Receptor.						
FT	SIGNAL	1	26	POTENTIAL_NICOTINIC_ACETYLCHOLINE_RECECTOR_SUBUNIT			
FT	CHAIN	27	494	DALPER6.			
SEQ	SEQUENCE	494 AA:	55980 MW;	4DF0572139587070 CRC64;			
Query Match		82.5%;	Score 2177;	DB 5;	Length 494;		
Best Local Similarity		81.6%;	Pred. No. 6-8e-198;				
Matches		35;	Mismatches	38;	Indels	20;	Gaps 3;
QY	2	APMLAAL-----LALLPVSEQQPHEKRLLNLLANTTLERPVANESEPLEYRFLGT	55	DR	PF02931;	Neur chan LBD;	1.
Db	3	SPLPASLSLFLVLLIAIKESCGQPHKERRQHLLNLSTYNTLERPVANESEPLEYRFLGT	62	DR	PF02932;	Neur_chan memb;	1.
QY	56	IQQIDVDEKNNLITNIWLSLENDYLNLPWNDSYEKGVKDLRTPNKLWKPDVLYNSA	115	DR	PRINTS; PR00252;	NRIONCHANNEL.	
Db	63	IQQIDVDEKNNLITNIWLSLENDYLNLPWNDSYEKGVKDLRTPNKLWKPDVLYNSA	122	DR	TIGR00860;	LIC;	1.
QY	116	DEGFDTGTYHISVWVKGSCLYVPPGKSTCMDIAWFPPDDQHCDMKGSWTYDGQL	175	DR	PROSITE; PS00236;	NEUROTRANSMITTER_CHANNEL;	1.
Db	123	DEGFDTGTYHISVWVKGSCLYVPPGKSTCMDITWFPPDDQHCEMKGSWTYDGQL	182	DR	Glycoprotein; Ionic channel;	Fos-synaptic membrane;	
QY	176	DLVLDKEAGGDLISDFITNGEYLLPDPGKNTIVTACPEYYDVDTITIRRRLYFF	235	DR	SEQUENCE; 509 AA;	57887 MW;	BED8E0198E02BD CRC64;
Db	183	DLVLSSEDGGDLISDFITNGEYLLPDPGKNTIVTACPEYYDVDTITIRRRLYFF	242	QY	2	APMLAAL-----LALLPVSEQQPHEKRLLNLLANTTLERPVANESEPLEYRFLGT	55
QY	236	NLIVPCVLISSWALGTLPPDSGKNTIVTACPEYYDVDTITIRRRLYFF	295	Db	3	SPPLASLSLFLVLLIAIKESCGQPHKERRQHLLNLSTYNTLERPVANESEPLEYRFLGT	62
Db	243	NLIVPCVLISSWALGTLPPDSGKNTIVTACPEYYDVDTITIRRRLYFF	302	QY	56	LQQIDV-----DEKNQNLITNIWLSLENDYLNLPWNDSYEKGVKDLRIT	100
QY	296	YFNCLIMFMVASSVVLTVVVLNYHRTADIHMPMIKSYFLQWLPWILMGRPRRKITRK	355	Db	63	LQQIDVDEKNNLITNIWLSLENDYLNLPWNDSYEKGVKDLRIT	122
Qy							

		Query Match Best Local Matches	Match Conservative 32;	Score Mi matches 39;	DB 5; Pred. No. 6.6e-196;	Length 49;	Gaps 4;
Db	123 PNLKWKEDDLMYNADEGGDFGTYTINIVKRSGSCLYYPGIFSTCKMDITWPFDDOCH 182						
Qy	161 CDMEFGSWYTDGNQQLDVLVDRDEAGGDLSDTFINGEWYLIGMPGKNTTITYACCEPEPYDV 220						
Db	183 CEMEFGSWYTDGNQQLDVLVNSEDGGDLSDTFINGEWYLAMPGKNTTITYACCEPEPYDV 242						
Qy	221 TFTMIRRLRLLYFFNLTVPCVLISSMALLGFTLPPDSGEKLTLGVTTILSVFLNVA 280						
Db	243 TFTQIIRRRLYFFNLTVPCVLISSMALLGFTLPPDSGEKLTLGVTTILSVFLNVA 302						
Qy	281 ETLPQVSDAIPPLGTYFNCIMMEMASSVYLTVVLYHRTADTHEPMQIKSYFLQMP 340						
Db	303 ETLPQVSDAIPPLGTYFNCIMMEMASSVYLTVVLYHRTADTHEPMWIKSVFLQMP 362						
Qy	341 WILMSRPQKKTAKTMMINTRPBELEKERSKSILLANVLDDDDFRHTADTHEPMWIKSVFLQMP 400						
Db	363 WILMGRPSPRKTKTLLSNRMKELELMERSKSILLANVLDDDDFRHTADTHEPMWIKSVFLQMP 415						
Qy	401 GNLSPGCSTFRTRFRSSVFRPSTMEDVGGGLSHREHLIGRELQFTARMKKADEAE 460						
Db	416 SQTAGSS-----ASFRSPRTVEHHATAIGCNHKDLILKEBLQFITARMKKADEAE 468						
Qy	461 LISDWKFAAMVVDREFCLFYFTLFTLIATAVVLSAPHTIVQ 501						
Db	469 LIGDWKFAAMVVDREFCLFYFTLFTLIATAVVLSAPHTIVQ 509						
<b>RESULT 7</b>							
Q8T7R9	PRELIMINARY;	PRT;	523 AA.				
ID	Q8T7R9						
AC	Q8T7R9;						
DT	01-JUN-2002 (TREMBLrel.)	21,	Created)				
DT	01-JUN-2002 (TREMBLrel.)	21,	Last sequence update)				
DT	01-JUN-2003 (TREMBLrel.)	24,	Last annotation update)				
DE	Nicotinic acetylcholine receptor Dalphag	subunit variant type V.					
GN	NACR-ALPHA-30D OR NACRALPHA-30D OR BCDDNA:GH01410	OR CG4128.					
OS	Drosophila melanogaster (Fruit fly).						
EC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;						
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;						
OC	Ephydriodea; Drosophilidae; Drosophila.						
NCBI_TAXID	=7227;						
RN	[1]						
RP	SEQUENCE FROM N.A. PubMed=21959411;						
RX	MEDLINE=21959411;						
RA	Grauso M., Reenan R.A., Culeto E., Sattelle D.B.;						
RT	"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,"						
RT	Dalphag, Dalphag and Dalphag. in Drosophila melanogaster Identify a						
RT	New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-co-I Pre-mRNA Editing";						
RL	Genetics 160:1519-1533 (2002).						
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).						
CC	-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.						
DR	EMBL: AF221449; AAM13396.1.						
DR	FLYBase: FBgn0032151; nAChR-alpha-30D.						
DR	GO; GO:0016021; C: integral to membrane; IEA.						
DR	GO; GO:0005330; P: extracellular ligand-gated ion channel activity; IEA.						
DR	GO; GO:0005216; P: ion channel activity; IEA.						
DR	GO; GO:0030594; P: neurotransmitter receptor activity; IEA.						
DR	GO; GO:0006811; P: ion transport; IEA.						
DR	InterPro; IPR006201; Neu chan LBD.						
DR	InterPro; IPR006202; Neu chan LBD.						
DR	InterPro; IPR006229; Neu chan memb.						
DR	PFam; PF02931; Neu chan_LBD; 1.						
DR	PFam; PF02932; Neu chan memb; 1.						
DR	PRINTS; PR00252; NATIONCHANNEL.						
DR	TIGRFAMs; TIGR00860; LIC; 1.						
DR	PROSITE; PS00236; NEUROTRION CHANNEL; 1.						
KW	Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;						
KW	Transmembrane.						
SQ	SEQUENCE 523 AA; 59110 MW; 1C200AAF74F87F841 CRC64;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	SEQUENCE FROM Berkeley;						
RX	Medline=20196006; PubMed=10731132;						
AC	Q9VLT79;						
DT	01-MAY-2000 (TREMBLrel.)	13,	Created)				
DT	01-OCT-2002 (TREMBLrel.)	22,	Last sequence update)				
DT	01-JUN-2003 (TREMBLrel.)	24,	Last annotation update)				
DE	C64128 protein.						
GN	NACR-ALPHA-30D OR NACRALPHA-30D OR BCDDNA:GH01410 OR CG4128.						
OS	Drosophila melanogaster (Fruit fly).						
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;						
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;						
OC	Ephydriodea; Drosophilidae; Drosophila.						
NCBI_TAXID	=7227;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	SEQUENCE FROM Berkeley;						
RX	Medline=20196006; PubMed=10731132;						
AC	Q9VLT79;						
DT	01-MAY-2000 (TREMBLrel.)	13,	Created)				
AManatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Henderson S.N., Sutton G.G., Wortsman J.P., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blaize R.G., Champé M., Pfeiffer B.D., George R.A., Lewis S.E., Richards S., Asbury M., Henderson S.N., Abrial J.P., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman D.P., Bhandari D., Bolshakov S., Borkovska D., Boettcher P., Brotkina P., Cadiou E., Cadieu F., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mys A.-D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Durkin P.,							

RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,	DR	PROSITE; PS00236; NEURON-ION CHANNEL, 1.
RA	Fosher A.E., Gabriele A.E., Gorrell J.H., Gu Z., Guan P., Harris M.,	SQ	SEQUENCE 554 AA; 63236_MW; DEC63E7F5B32A35 CRC64;
RA	Glock A., Gong F., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	Query	Match 69.4%; Score 1833; DB 5; Length 554;
RA	Harris N.L., Houston T.J., Ibeagwam C., Jaijali M., Kalush F., Karpov G.N., Ketchum K.A.,	Best Local Similarity	65.0%; Pred. No. 4e-165;
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	Matches	370; Conservative 36; Mismatchs 67; Indels 96; Gaps 8;
RA	Lasho P., Lei Y., Levitan A.A., Li J., Li Z., Liang Y., Lin X.,	Qy	4 MIAAIALLPVSGQPHBKRLNLLANVNTLERYVANESELEVRGLTQQIIDVD 63
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	Db	11 LFVLILFLAIKESCGQPHBKRLNLLSTYNTLERYVANESELEVRGLTQQIIDVD 70
RA	Merkulov G., Mil'shina N.V., Mobarry C., Morris J., Moshrefi A.,	Qy	64 EKNQQLITNIWLSLEWNDYLWNDESEYGVVKDURITPNKLWEDVLMNSADGFGDTY 123
RA	Mount S.M., Moy M., Murphy L., Muzny D.M., Nelson D.L.,	Db	71 EKNQQLITNIWLSLEWNDYLWNDESEYGVVKDURITPNKLWEDVLMNSADGFGDTY 130
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,	Qy	124 QTNNYVRSQGSCLVPPGIFKSTCKMDIAWFPEDDQHUCMKFGSWTYDNQDLYVKEA 183
RA	Palaiozio M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	Db	131 HTNIVVKHNGSCLVPPGIFKSTCKMDIAWFPEDDQHUCMKFGSWTYDNQDLYVNESED 190
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shan H.,	Qy	184 GGDSLDFITNGEWNLIGM-PGKNTNTYACCP-----EPYDVDTFTIMIRR 229
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,	Db	191 GGDSLDFITNGEWNLIGM-PGKNTNTYACCP-----GGTLPPDSGEKLT----- 239
RA	Spier B., Spradling A.C., Stapleton M., Strong R., Sun F., Wang X.,	Qy	230 TLYYFENLTVPCVLTSMALL----GGTLPPDSGEKLT----- 263
RA	Svirskis R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	Db	240 ILPFOENCAMCANLIDGPGLHAAAGFRETDAGRNYTTINSISKPCRRVHAIDNVGCCS 299
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	Qy	264 -----LG-----VILLISITVFNLVAETLPQSDAIP 292
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	Db	300 SYRTHFTILKRYSKYKGPIORTDHYQCPAERTVILLISITVFNLVAETLPQSDAIP 359
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	Qy	293 LGTYENCIMMVASSVVLTVVLYNTHRTADHMPWIKSVFELWLPWIRMSMRPGKKI 352
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RT	Db	360 LGTYENCIMMVASSVVLTVVLYNTHRTADHMPWIRMSMRPGKKI 419
RA	"The genome sequence of <i>Drosophila melanogaster</i> ."; [2]	Db	355 TRKTINMNTNRELEDKERSSKLIANVLDIDDPHRGPPPNASTGNLPGGSIFRT 412
RA	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	Qy	420 TRKTILLSNRMKKELEKERSSSKLIANVLDIDDPFRH-----TISGSOAIGSS--- 468
RA	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	Db	413 DFRKFVPTMEYDGCGIOSHHLHLTRELQITARNRKADDDEAELISDWKPAAMVV 472
RA	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	Db	469 --ASGRPTVEEHTAIGCNHDQJHLIKELOFTARNRKADDDEAELIGDWKPAAMVV 525
RA	SEQUENCE FROM N.A.	Qy	473 DRFCFLVFVFTLTIATVAVLSSPHIIV 501
RA	Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,	ID	Q9XZ13 PRELIMINARY; PRT; 496 AA.
RA	Evans C.A., Gocayne J.D., Amanatides P.G., Branden R.C., Rogers Y.,	AC	526 DRFCFLVFVFTLTIATVAVLSSPHIIVQ 554
RA	Banzon D., Baldwin J., An H., Besson K.Y., Busam D.A.,	DB	526 DRFCFLVFVFTLTIATVAVLSSPHIIVQ 554
RA	Carlson J.W., Center A., Champé M., Davenport L.B., Dietz S.M.,	RESULT	9
RA	Dodson K., Dorsett V., Doup L.E., Doyle C., Dreaneck D., Farfan D.,	Q9XZ13	DRFCFLVFVFTLTIATVAVLSSPHIIV 501
RA	Ferreria S., Frise B., Galie R.F., Garg N.S., George R.A.,	AC	526 DRFCFLVFVFTLTIATVAVLSSPHIIVQ 554
RA	Gonzalez M., Houck J., Hopkins R.A., Hostin D., Howland T.J.,	DT	01-NOV-1999 (TREMBrel 12, Created)
RA	Ibeagwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,	DT	01-NOV-1999 (TREMBrel 12, Last sequence update)
RA	McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,	DT	01-JUN-2003 (TREMBrel 24, Last annotation update)
RA	Pacleb J., Paraga V., Park S., Patel S., Pfeiffer B.,	DE	Putative nicotinic acetylcholine receptor alpha 7-1 subunit.
RA	Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,	OS	Heliothis virescens (Noctuid moth) (Owlie moth).
RA	Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,	OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Glossata; Dipterygia; Noctuoidea;
RA	Williams S.M., Zaveri J.S., Shu S., Smutniak F., Whitfield E.,	OC	Noctuidae; Heliothinae; Heliothis.
RA	"Sequencing of <i>Drosophila melanogaster</i> genome.";	RN	[1]
RA	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	RP	SEQUENCE FROM N.A.
RA	Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,	DR	Adamczewski M., Adamczewski M., Oellers N., Oellers N.,
RA	Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,	DR	Schulte T., Schulte T.,
RA	Clamp M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N.,	DR	"Putative alpha subunits of insect nicotinic acetylcholine receptors
RA	Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,	DR	more similar to vertebrate alpha 7 subunits and <i>C. elegans</i> Ce21 than
RA	Searle S.M.J., Smith E., Shu S., Smutniak F., Whitefield E.,	DR	other insect nicotinic acetylcholine receptor alpha subunits."
RA	Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;	DR	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RA	RT	CC	-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
RA	"Annotation of <i>Drosophila melanogaster</i> genome.";	DR	-- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
RA	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.	DR	EMBL; AF143846; AAD26971; -.
RA	SEQUENCE FROM N.A.	DR	GO: GO:0016020; C:membrane; I:alpha-3D0.
RA	Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;	DR	INTERPRO: IPR000202; Neur_chan LBD.
RA	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	DR	INTERPRO: IPR000202; Neur_chan LBD.
RA	SEQUENCE FROM N.A.	DR	INTERPRO: IPR000202; Neu_chan memb.
RA	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.	DR	PFam; PF02931; Neur_chan LBD; I.
RA	SEQUENCE FROM N.A.	DR	PRINTS; PR00252; NRIONCHANNEL.
RA	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.	DR	TIGRFAMS; TIGR00860; LIC; 1.
RA	SEQUENCE FROM N.A.	DR	GO: GO:0005230; F:extracellular ligand-gated ion channel acti. . . ; IEA.
RA	SEQUENCE FROM N.A.	DR	GO: GO:0005232; Neur_chan memb; 1.
RA	SEQUENCE FROM N.A.	DR	GO: GO:0016021; C:integral to membrane; IEA.
RA	SEQUENCE FROM N.A.	DR	GO: GO:0005230; F:extracellular ligand-gated ion channel acti. . . ; IEA.

DR	GO; GO:0005216; F:ion channel activity; IEA.	RA	Millar N.S.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR	GO; GO:0006811; P:neurotransmitter receptor activity; IEA.	RL	EMBL; AU54210; CAP8693-1; -
DR	GO; GO:0007268; P:synaptic transmission; IEA.	DR	DR
DR	InterPro; IPR06201; Neur channel.	DR	GO; GO:0016020; C:membrane; IEA.
DR	InterPro; IPR06202; Neu chan LBD.	DR	GO; GO:0005230; P:extracellular ligand-gated ion channel acti. - ; IEA.
DR	InterPro; IPR06029; Neu _channel_memb.	DR	GO; GO:0030594; P:neurotransmitter receptor activity; IEA.
DR	Pfam; PF02932; Neu chan LBD; 1.	DR	GO; GO:0006811; P:ion transport; IEA.
DR	Pfam; PF02932; Neu chan memb; 1.	DR	InterPro; IPR06201; Neur_channel.
DR	PRINTS; PR00252; NEURONCHANNEL.	DR	InterPro; IPR06202; Neur_chan_LBD.
DR	TIGRFAMS; TIGR0866; LIC; 1.	DR	InterPro; IPR06029; Neu_Channel_memb.
DR	PROSITE; PS00236; NEURO_IION CHANNEL; 1.	DR	Pfam; PF02931; Neur_chan_LBD; 1.
KW	Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Transmembrane.	DR	PRINTS; PR00252; NEURONCHANNEL.
SQ	SEQUENCE 496 AA; 56341 MW; 8032FED8515A6210 CRC64;	DR	TIGRFAMS; TIGR0860; LIC; 1.
Query Match	68.3%; Score 1803.5; DB 5; Length 496;	DR	PROSITE; PS00336; NEURO_IION_CHANNEL; 1.
Best Local Similarity	68.7%; Pred. No. 2.2e-162;	KW	Signal; Receptor.
Matches	347; Conservative 53; Mismatches 78; Indels 27; Gaps 7;	FT SIGNAL	68.2%; Score 1801.5; DB 5; Length 542;
Qy	2 APMLAALALLLPVSEQ-GPHEKRLLNALLANYNTLEPPVANESEPLFVRFGTLQQI 60	FT CHAIN	Best Local Similarity 65.5%; Pred. No. 3.9e-162;
Db	12 APAGLILCLLWPGARGCYHEKRLLHHLDDHNVLEPPVANESEPLDPLSFGHTLMQI 71	FT CHAIN	Mismatches 59; Mismatches 79; Indexes 45; Gaps 5;
Qy	61 DVDEKNQLLITNWLSELENDYNEFLRNDSSEYGGYKVDLRLRTPNKLWKPDTLYMNSADEGFD 120	SQ	SEQUENCE 542 AA; 60988 MW; 69D2C39746BB74D7 CRC64;
Db	72 DVDEKNQLLITNWLSELENDYNEFLRNDSSEYGGYKVDLRLRTPNKLWKPDTLYMNSADEGFD 131	Qy	4 MLAALIALLLPVSEQGPHEKRLLNALLANYNTLEPPVANESEPLFVRFGTLQQI DWD 63
Qy	121 GTQTNVYVRSGGSCLYVPGIFKSTCKMDIAWPFDDHCDMKFGSWTYDGNQQLDVLV 180	Db	20 LVSEGJLQSLPAGAPEKRLLHALLDYNSLERPVNESEPLQLSFGLTLMQI DWD 79
Db	132 STYPTNVRVTRNGSCLYVPGIFKSTCKDITWPFDDQRCRNKEKGWSWYDGYQQLDQLQI 191	Qy	64 EKNQLLITNWLSELENDYNLRNDSSEYGGYKVDLRLRTPNKLWKPDTLYMNSADEGFDGTY 123
Qy	181 DEAGDLSFIFTINGEWYLGMGPGEKNTTITYACCEPEPYVDTFTIMIRERTLXXFFNLIYP 240	Db	80 EKNQLLITNWLSELENDYNLRNDSSEYGGYKVDLRLRTPNKLWKPDTLYMNSADEGFDGTY 139
Db	192 DEGGDISSFEVTNGEWYLGVPGKRNENYNCCPEPYVDTFTAVIRRTLXXFFNLIYP 251	Qy	124 QINVVVRSGSGSCLYVPGIFKSTCKMDIAWPFDDHCDMKFGSWTYDGNQQLDVLVDEA 183
Qy	241 CVLISMALLGFTLPPDSEKELTGYTILLSLTVFLNVAETLQPQVSDAIPLLGTYENCI 300	Db	140 ATNVVWRNRINGSCLYVPGIFKSTCKDITWFPDDQRCBNMFQSLDFQFLQJLQLQDEA 199
Db	252 CVLISMALLGFTLPPDSEKELSGLVTTSLTVFLNVAETLQPQVSDAIPLLGTYENCI 311	Qy	184 GGDLSDFTINGEWYLGMGPKNNTITYACCEPEPYVDTFTIMIRERTLXXFFNLIYPVYL 243
Qy	301 MFMVASSVLTVVVNYHRTADIHMPWIKVSYFLOWLPWILMSRPGKLTTRKTIMMN 360	Db	200 GGDLSFTINGEWYLGMGPKNNTITYACCEPEPYVDTFTIMIRERTLXXFFNLIYPVYL 259
Db	312 MFMVASSVSTLIVNYHRTADHTHEMSDWIRCVFYLWLPWILMSRPGSATTPPPARV- 370	Qy	244 ISSMALLGFTLPPDSEKELTGYTILLSLTVFLNVAETLQPQVSDAIPLLGTYENCI MF 3.03
Qy	361 TRMRELELKERSKSLLANVLDDDFRHGPPPNSTAGNLGPGCSTFRDFRSFVR 420	Db	260 IASMALLGFTLPPDSEKELSGLVTTSLTVFLNVAETLQPQVSDAIPLLGTYENCI MF 3.19
Db	371 PPPDLELRERSKSLLANVLDDDFRHGPPPNSTAGNLGPGCSTFRDFRSFVR 414	Qy	304 VASSVLTVVVNYHRTADIHMPWIKVSYFLOWLPWILMSRPGKLTTRKTIMMN 352
Qy	421 PSTMEDVGGLGSH----HRELHLILRELOFTTARMKKADEPAAELISDWKPAAMVYDRL 475	Db	320 VASSVSTLIVNYHRTADHTHEMSDWIRCVFYLWLPWILMSRPGSATTPPPSSS 379
Db	415 ---EENGAGLAHNSCFGYDYESLILKIRVTDQRRDDEADISRWKPAAMVYDRL 470	Qy	353 TRKTMNTRMRELELKERSKSLLANVLDDDFRHGPPPNSTAGNLGPGCSTFR 412
Qy	476 CLFVFETLFTIATAVLISAPHIV 500	Db	380 SSASGEKKQQIQNLVKEERSKSLLANVLDDDFRHGPPPNSTAGNLGPGCSTFR 434
Db	471 CLIFTLFTIATAVLISAPHIV 495	Qy	413 DFRSFYRPSMID-----VGGGL -----GSHHRHLHLIRELQDITA 450
Db	435 MYRGQ-----DDGSYGVGPAGPYDVGRLHEAISHTCLTSSAEYELALIKEWMITE 487	Qy	451 RMKKADEBAELISDWKPAAMVYDRCFLFTIATAVLISAPHIV 500
RESULT 10	Q86MN7 PRELIMINARY; PRT; 542 AA.	ID	Q8T7V5 PRELIMINARY; PRT; 807 AA.
Q86MN7	PRELIMINARY;	AC	Q8T7V5 PRELIMINARY; PRT; 807 AA.
DT 01-JUN-2003 (TREMBLrel. 24, Created)	DT 01-JUN-2002 (TREMBLrel. 21, Created)	AC	Q8T7V5 PRELIMINARY; PRT; 807 AA.
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)	AC	Q8T7V5 PRELIMINARY; PRT; 807 AA.
DE Nicotinic acetylcholine receptor subunit Dalpha7 precursor.	DE Nicotinic acetylcholine receptor subunit Dalpha7 precursor.	AC	Q8T7V5 PRELIMINARY; PRT; 807 AA.
NACRALPHA-1BC.	NACRALPHA-1BC.	AC	Q8T7V5 PRELIMINARY; PRT; 807 AA.
Drosophila melanogaster (Fruit fly).	Drosophila melanogaster (Fruit fly).	AC	Q8T7V5 PRELIMINARY; PRT; 807 AA.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	AC	Q8T7V5 PRELIMINARY; PRT; 807 AA.
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	AC	Q8T7V5 PRELIMINARY; PRT; 807 AA.
OC Drosophilidae; Drosophila; Drosophila.	OC Drosophilidae; Drosophila; Drosophila.	AC	Q8T7V5 PRELIMINARY; PRT; 807 AA.
NCBI_TAXID=227;	NCBI_TAXID=227;	AC	Q8T7V5 PRELIMINARY; PRT; 807 AA.
RN SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.	AC	Q8T7V5 PRELIMINARY; PRT; 807 AA.
OS Drosophila melanogaster (Fruit fly).	OS Drosophila melanogaster (Fruit fly).	AC	Q8T7V5 PRELIMINARY; PRT; 807 AA.

OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC	Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBI_TAXID=7227;	Drosophila; Drosophilidae; Drosophila.
[1]	
RN	SEQUENCE FROM N.A. MEDLINE=11969411; PubMed=11973307;
RX	GRAUSO M., REENAN R.A., CULETTO E., SATTELLE D.B.; Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes Dalphas, Dalphas6 and Dalphas7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing. ";
RT	Genetics 160:1519-1533 (2002).
RT	-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
RL	EMBL; AF272778; AAM13390.1 ;
DR	FlyBase; FBgn00288975; nacr-alpha-34E.
DR	GO; GO:0016021; C-integral to membrane; IEA.
DR	GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . . ; IEA.
DR	GO; GO:0005216; F:ion channel activity; IEA.
DR	GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR	GO; GO:0006811; F:ion transport; IEA.
DR	INTERPRO; IPR006206; P:synaptic transmission; IEA.
DR	INTERPRO; IPR006201; Neur_chan_LBD.
DR	INTERPRO; IPR006002; Neur Chan_LBD.
DR	INTERPRO; IPR006029; Neu_Channel_memb.
DR	PFAM; PF02931; Neu chan_LBD; 1.
DR	PFAM; PF02932; Neu chan_memb; 1.
PRINTS	PR00232; NRIONCHANNEL.
DR	TIGRFAMS; TIGR000860; LIC: 1.
DR	PROSITE; PS00235; NEUROTRION CHANNEL; 1.
DR	Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Transmembrane.
SQ	SEQUENCE 807 AA; 91223 MW; C8BAFB342879C8 CRC64;
Query Match	Score 1800.5; DB 5; Length 807;
Best Local Similarity	66.3%; Pred. No. 8.6-162;
Matches	348; Conservative 61; Mismatches 69; Indels 47; Gaps 9;
QY	10 LLALLPVSQ --GPHEKRLNLLANMNTLERYVANESEPLEPTFREGLTQLQIIVDEK 65
DB	295 LLIYLVNLISAKVCLAGYHEKLRLHDLPDNTLERYPLVNESENPLQLSFQLTQMQLQIIVDEK 354
QY	66 NQLLTINWLSLEWDNLNRANDNSENGVQDLDLRTPNKLWPKDVLMYNSADEGFDGTQYQT 125
DB	355 NQLLTVNWNLKLENDMLNLKNTSDYGGVQDLRIPPRINKPDVLYNSADEGFDGTQYQT 414
QY	126 NVVVRSGSCSLVYPGPFGKSTCMDIAWFPPDDQHCDMKFGWSWTYDGNQDLVLDDEAGG 185
DB	415 NVVVRNGSCSLVYPGTFKSTCKDIDTWFPDDQRCZEMKFGWSWTYDGFQDLQLQDGTGG 474
QY	186 DLSDFTINGENYLIGMKGKNTTVAACCPPEPYDVFITMRRTLYFFFLVPLVYLIS 245
DB	475 DISSYVNGEWLLGVYKBRYYNCVCPVTDITFAIIRRRTLYFFFLVPLVYLIA 534
QY	246 SMALLGFTLPPDSGEKLTGLGYTILLSLTIVLNIVATPLQVSDAIPLGLYFNCFIMFMVA 305
DB	535 SMALLGFTLPPDSGEKLTGLGYTILLSLTIVLNIVATPLQVSDAIPLGLYFNCFIMFMVA 594
QY	306 SSVVLTIVVNLNYHTRDATHMPWIKSVLVEQWLPLWMSRPGKTKRK--TIMMNTR 362
DB	595 SSVVSTLILNYHTRDATHMSEWIRVELCWLPNPLWMSRPGRPLILEFPTPCSDTS 654
QY	363 -----MRELELKERSKSLLANVLDIDDDFRHG----PPPNSTASGNLGPGCSLFRTD 413
DB	655 SERKHQLSDVEKRSKSLLANVLDIDDERHNCRPMTPS----GTLSHNPAYRTV 709
QY	414 FRRSFVPRSTMDVG--GGLGS-----HHR-----ELHLTLRELQFITARMKK 455
DB	710 YGGG-----DDGSCIGPGRMSPDAVHTCIRSTEYBLGLIKEITRFITDQRKD 761
QY	456 DEBAELLSDWKEKAMVYDFRCLEVTFITIATVAVLSSAPHIV 500

RA	Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of <i>Drosophila melanogaster</i> genome." ; Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	QY	467 FAAMTVDRFLFLVFTLFTIATVAVLLSAPHIIV 500
RN	[3]	Db	507 FAAMTVDRCLLIFTLFTIATVAVLLSAPHFIV 540
RP	SEQUENCE FROM N.A.		
RA	Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Prochnik S.E., Smith C.D., Tupy J., Huang Y., Kaminker J.S., Carlson B., Celniker S.E., Berman B., Carlson J.W., de Celniker P., Clamp M., Drysdale R., Emmert D., Frise E., Grey A., Harris N., Krommiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of <i>Drosophila melanogaster</i> genome." ; Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	RESULT 1.3	
RA	[4]	Db	Q81E2; PRELIMINARY; ID Q81E2; AC Q81E2; DT 01-MAR-2003 (TREMBLrel. 23, Created); DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update); DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
RA	RP	DE CG4128-PC; GN NACR-ALPHA-300 OR NACRALPHA-30D OR BCDDNA: GH01410 OR CG4128.	
RA	OS Drosophila melanogaster (Fruit fly).	OS	
RA	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.	OC	
RA	NCBI_TaxID:7227; OX NCBI_TaxID:7227;	OC	
RA	RP	SEQUENCE FROM N.A.	
RA	Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; "Annotation of <i>Drosophila melanogaster</i> genome." ; Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	RP	SEQUENCE FROM N.A.
RA	[5]	Db	SEQUENCE FROM N.A.
RA	RP	SEQUENCE FROM N.A.	
RA	RP	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AB03511; AF48950.2; -	DR	EMBLINE:2019606; PubMed=10731132;
DR	FlyBase; FBgn0031014; nACR-alpha-18C.	DR	RX Adams M.D., Celniker S.E., Holt R.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazej R.G., Champé M., Pfieffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L., Abrial J.P., Agbayani A., Hahn H.J., Andrews-Pfannkoch C., Baldwin D., Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borrova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport J.B., Davies P., de Pablo B., Delcher A., Deng Z., May S.A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Duran-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabril A.B., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lasko P., Leibl Y., Levitt A.A., Li J., Li Z., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Miashina N.V., Mobarry C., Morris J., Moskrefi A., Mount S.M., Moy M., Murphy B., Muzyzny D.M., Nelson D.L., Nelson D.R., Nixon K., Nixon K., Nusslein D.R., Pacieb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Purvi V., Reese M.G., Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H., Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Svartman R., Tector C., Turner R., Venter C., Weinstock G.M., Wasserman D.A., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zheng L., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of <i>Drosophila melanogaster</i> ." ; Science 287:2185-2195 (2000). [2]
RA	RP	SEQUENCE FROM N.A.	
RA	Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Evans C.A., Gooley J.D., Amanatides P.G., Brandon R.C., Rogers Y., Banzon J., An H., Baldwin D., Beeson J., Busam D.A., Carlson J.W., Center A., Champé M., Davenport L.B., Dietz S.M., Dorsett V., Doup L.E., Doyle C., Dresmek D., Farfan D., Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Kruse D., Li P., Mathee B., Moskrefi A., Ibegwam C., Jalali M., McInroy T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., Pacieb J., Paragas V., Park S., Patel S., Pfieffer B.,		

RA	Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Swirskas R., Tector C., Tyler D., Wilkins S.M., Zaveri J.S., Smith H.C., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome.";	Db	411 SKSLANVLDIDDDERH-----TISGSQTAIGSS-----ASFGRPTTVEEHHTAIG 456
RA	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.	QY	433 SHIREBLHLILREOFITARMKQADDEAEELISDWMKAAMVYDRFLFVFTLFTIATVAVL 492
RA	[3]	Db	457 CNHDLHLILKEOFITARMRKADDEAEELIGDWKFAAMVYDRFLFVFTLFTIATVTVL 516
RN	SEQUENCE FROM N.A.	QY	493 LSAPHIIIVQ 501
RP	Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kroymiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome.";	Db	517 LSAPHIIIVQ 525
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.	RESULT 14	Q9JHD6 ID: Q9JHD6 PRELIMINARY; PR7; 502 AA.
RN	SEQUENCE FROM N.A.	Q9JHD6 AC: Q9JHD6 DT: 01-OCT-2000 [TREMBrel. 15, Created)	AC: Q9JHD6 DT: 01-OCT-2000 [TREMBrel. 15, Last annotation update)
RP	Adams M.D., Celinker S.E., Gibbs R.A., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.	DT: 01-JUN-2003 [TREMBrel. 24, Last annotation update)	DT: 01-JUN-2003 [TREMBrel. 24, Last annotation update)
RL	[5]	DE Nicotinic acetylcholine receptor subunit alpha 7.	DE Nicotinic acetylcholine receptor subunit alpha 7.
RN	SEQUENCE FROM N.A.	GN: CHRNA7.	GN: CHRNA7.
RP	Flybase;	OS: Mus musculus (Mouse)	OS: Mus musculus (Mouse)
RA	Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.	RC: Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; NCBI_TaxID:10090;	RC: Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; NCBI_TaxID:10090;
RL	EMBL; AE031626; AAC10709.1; -.	RN: [1] -	RN: [1] -
DR	FlyBase; FBgn0032151; nacr-alpha-30D.	RP: SEQUENCE FROM N.A.	RP: SEQUENCE FROM N.A.
DR	GO: GO:0016020; C:extracellular ligand-gated ion channel acti. . . ; IEA.	RC: STRAIN=DA/210sg;	RC: STRAIN=DA/210sg;
DR	GO: GO:0005230; F:extracellular ligand-gated ion channel acti. . . ; IEA.	RX: MEDLINE=9037516;	RX: MEDLINE=9189245; PubMed=9037516;
DR	GO: GO:0030594; F:neurotransmitter receptor activity; IEA.	Stitzel J.A., Fairman D.A., Collings A.C.;	Stitzel J.A., Fairman D.A., Collings A.C.;
DR	GO: GO:0006811; P:ion transport; IEA.	"Linkage of strain-specific nicotinic receptor alpha 7 subunit restriction fragment length polymorphisms with levels of alpha-7 bungarotoxin binding in brain."	"Linkage of strain-specific nicotinic receptor alpha 7 subunit restriction fragment length polymorphisms with levels of alpha-7 bungarotoxin binding in brain."
DR	InterPro; IPR006201; Neur_channel.	RT: Brain Res. Mol. Brain Res. 43:30-40(1996).	RT: Brain Res. Mol. Brain Res. 43:30-40(1996).
DR	InterPro; IPR006202; Neur_chan_LBD.	RL: Brain Res. Mol. Brain Res. 43:30-40(1996).	RL: Brain Res. Mol. Brain Res. 43:30-40(1996).
DR	InterPro; IPR006029; Neu_Channel memb.	RN: [2]	RN: [2]
DR	Pfam; PF03931; Neur_chan_LBD; 1.	RP: SEQUENCE FROM N.A.	RP: SEQUENCE FROM N.A.
DR	Pfam; PF03932; Neu chan memb; 1.	RC: STRAIN=DA/210sg;	RC: STRAIN=DA/210sg;
DR	PRINTS; PRO00252; NRIONCHANNEL.	RA: Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.	RA: Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR	PROSITE; PS00236; NEUROTRANSMITTER CHANNEL; 1.	CC: -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN	CC: -1- SIMILARITY: BELONGS TO THE LIGAND-GATED ION CHANNEL FAMILY.
SQ	SEQUENCE 525 AA; 60135 MW; CF95283C56EA90A9 CRC64;	CC: EMBL; AF225980; AAF55885.1; -.	CC: EMBL; AF225980; AAF55885.1; -.
Query Match	64.6%; Score 1705.5; DB 5; Length 525;	DR: MGI: 99779; Chnra7.	DR: MGI: 99779; Chnra7.
Best Local Similarity	63.2%; Pred. No. 4.9e-153;	DR: GO: 0016021; P:ion transport; IEA.	DR: GO: 0016021; P:ion transport; IEA.
Matches	347; Conservative 43; Mismatches 84; Indels 75; Gaps 9;	DR: GO: 0005230; F:extracellular ligand-gated ion channel acti. . . ; IEA.	DR: GO: 0005230; F:extracellular ligand-gated ion channel acti. . . ; IEA.
QY	2 APMALAAI-----LALLPVSEQQGPHEKRLLNALLANINTLERPANESEPLEYRFLGLT 55	DR: GO: 000594; P:neurotransmitter receptor activity; IEA.	DR: GO: 000594; P:neurotransmitter receptor activity; IEA.
Db	3 SPLPASLISFLVLIFLAIKTESQGPHEKRLLNLLSYNTLERPANESEPLEYRFLGLT 62	DR: GO: 0006811; P:ion transport; IEA.	DR: GO: 0006811; P:ion transport; IEA.
QY	56 LQQIIPDVDEKNOLLITNLWLSLEWDNYLNRLDSEYYGGVQLDRITPNKLWRPDVLMYNSA 115	DR: GO: 0007268; P:synaptic transmission; IEA.	DR: GO: 0007268; P:synaptic transmission; IEA.
Db	63 LQQIIPDVDEKNOLLITNLWLSLEWDNNRLNNETYEGGVQLDRITPNKLWRPDVLMYNSA 122	DR: InterPro; IPR006202; Neu_Channel.	DR: InterPro; IPR006202; Neu_Channel.
QY	116 DEGFEDTYCOTNVYVRSGSCLXYPPGIFKSTKMDIAWFPPDDQHCDMKFESWTYDGNQL 175	DR: InterPro; IPR006029; Neu_Channel_memb.	DR: InterPro; IPR006029; Neu_Channel_memb.
Db	123 DEGFDTGYHTNIVKVRNGSCLYPPGIFKSTKIDTFPPDDQHCDMKFESWTYDGNQL 182	DR: Pfam; PF02932; Neu chan memb; 1.	DR: Pfam; PF02932; Neu chan memb; 1.
QY	176 DLVLDKEAGGDLSDFTINGENWYLMG_PKGKNTITYACCP-----EPYDVT 221	DR: PRINTS; PRO0052; NRIONCHANNEL.	DR: PRINTS; PRO0052; NRIONCHANNEL.
Db	183 DLVLSSEDDGDLSDFTINGENWYLMG_PKGKNTITYACCP-----EPYDVT 221	DR: PROSITE; PS00236; NEUROTRANSMITTER CHANNEL; 1.	DR: PROSITE; PS00236; NEUROTRANSMITTER CHANNEL; 1.
QY	222 FTIMIRRTLYTFENLIVPCVLISSMALL---GFTIUPPDSEKLTGIV----- 266	DR: Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; KW Transmembrane.	DR: Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; KW Transmembrane.
Db	240 -----ILFFQFNCAACNLIDGP7GLHIAAGFGETDAGRNYTILINSISKPCRVRH 291	SQ: SEQUENCE 502 AA; 56617 MW; C9353E5136620B3 CRC64;	SQ: SEQUENCE 502 AA; 56617 MW; C9353E5136620B3 CRC64;
QY	267 -----TILISLITVFLNLTAETLPQVSDAIPLIGTYFNCTIMENVASSVLT 312	Query Match Best Local Similarity 4.7%; Score 1258.5; DB 11; Length 502;	Query Match Best Local Similarity 4.7%; Score 1258.5; DB 11; Length 502;
Db	292 ADNVGCCSRYTHTILKRYSLXKYGPGRFTIDHYQ_C-RAESTYFNCTIMENVASSVLT 350	DB: 10 LAIAAALLHVSIQEFORLKYKEVLYNYPLEPVANSOPDQVTSVYFSLSLQIMDYDEK 69	DB: 10 LAIAAALLHVSIQEFORLKYKEVLYNYPLEPVANSOPDQVTSVYFSLSLQIMDYDEK 69
QY	313 VVLYNHHTADTHEMPQWIKSYFLQWLFILWLRNGRPRKTKTILLSNRMKBEELERS 372	QY: 67 QLJITNWLSLFWNDYLNRLWDSYEYGGVKDLRITPNKLWPKDVLMLNSADEGFDTGTYQTN 126	QY: 67 QLJITNWLSLFWNDYLNRLWDSYEYGGVKDLRITPNKLWPKDVLMLNSADEGFDTGTYQTN 126
Db	351 VVLYNHHTADTHEMPWIKSYFLQWLFILWLRNGRPRKTKTILLSNRMKBEELERS 410	DB: 70 QVTTTNTWLMQSWTDYLOWNNSSEPVKAVRFPDGQWIKPILLNSADERDATHTN 129	DB: 70 QVTTTNTWLMQSWTDYLOWNNSSEPVKAVRFPDGQWIKPILLNSADERDATHTN 129
QY	373 SKSLANVLDIDDDFRHGPVPNSTASTGNGLPGCGS1FRTDFRRSFYRPSTMEDVGGLG 432	QY: 127 VVTRSGSSCLYVPPGIFKSTKMDIAWFPPDDQHCDMKFESWTYDGNQLDLVLKDEACGD 186	QY: 127 VVTRSGSSCLYVPPGIFKSTKMDIAWFPPDDQHCDMKFESWTYDGNQLDLVLKDEACGD 186



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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 8, 2004, 11:50:34 ; Search time 3498.21 Seconds  
 (without alignments)  
 4276.744 Million cell updates/sec

Total number of hits satisfying chosen parameters: 55026578

Post-processing: Minimum Match 0%

Maximum Match 0%

Listing first 45 summaries

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 0%

Listing first 45 summaries

Command line parameters:

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-Q /cgn2_1/ISPTO_spool/US0930323/runat_07052004_101110_23893/app_query.fasta_1.2261
-DB=EST -QFMM=faslap -SUFFIX=rst -MINMATCH=0.1 -LOOPBXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DALIGN=200 -THR SCORE=pct THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMM=pfo -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000000
-USER=US0930323 @CGN 1.4577 @runat 07052004_101110_23893 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG -SCORE=0 -WAIT -DSPBLOCK=10 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=0 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELPOP=6 -DELEXT=7
```

Database :

EST: \*

```
1: em_estba:*
2: em_estbm:*
3: em_estin:*
4: em_estm:*
5: em_estov:*
6: em_estp1:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_p1n:*
20: em_gss_vrc:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rdc:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gssi:*
```

29: gb\_gssi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
c 1	1273	48.2	885	12	BG632919	GH16126.3	
c 2	970.5	36.8	1864	11	AK053497	Mus muscu	
c 3	970.5	36.8	2916	11	AK051730	Mus muscu	
c 4	970.5	36.8	3126	11	AK00415	Mus muscu	
c 5	957.5	36.3	1436	29	AY402873	Homo sapi	
c 6	944.5	35.8	1436	29	AY402875	Mus muscu	
c 7	924	35.0	2010	11	AK080475	Mus muscu	
c 8	922.5	34.9	2296	14	CD013901	90124548	
c 9	914	34.6	1454	29	AY402878	Mus muscu	
c 10	910.5	34.6	4037	11	AK049722	Mus muscu	
c 11	910.5	34.5	4046	11	AK051742	Mus muscu	
c 12	909	34.4	1201	9	AL530299	AL530299	
c 13	905	34.3	1374	29	AY406230	Homo sapi	
c 14	890.5	33.7	2940	11	AK034228	Mus muscu	
c 15	890.5	33.7	3230	11	AK083157	Mus muscu	
c 16	886.5	33.6	4290	11	AK029177	Mus muscu	
c 17	886	33.6	1374	29	AY406232	Mus muscu	
c 18	884	33.5	1442	29	AY406233	Homo sapi	
c 19	882.5	33.4	1781	14	CD013889	CD013889	
c 20	881	33.4	1442	29	AY402877	Pan trogl	
c 21	865.5	32.8	1374	29	AY406231	Pan trogl	
c 22	853	32.3	4589	11	AK030464	Mus muscu	
c 23	849	32.2	922	13	BU915857	AGENOCOURT	
c 24	847	32.1	607	9	AI292581	GH1518.5	
c 25	846.5	32.1	1436	29	AY402874	Pan trogl	
c 26	838.5	31.8	3483	11	AK081254	Mus muscu	
c 27	791.5	30.0	1466	14	CD013891	CD013891	
c 28	776.5	29.4	2257	11	AK017571	Mus muscu	
c 29	770	29.2	1751	14	CD013905	CD013905	
c 30	770	29.2	2110	14	CD013902	CD013902	
c 31	770	29.2	2110	14	CD013903	CD013903	
c 32	770	29.2	2513	11	AK033068	Mus muscu	
c 33	769.5	29.1	2074	11	AK087554	Mus muscu	
c 34	759	28.7	908	13	BU149265	AGENOCOURT	
c 35	748.5	28.4	1034	13	BX403124	BX403124	
c 36	737.5	27.9	1596	14	CD013888	90138806	
c 37	716	27.1	1603	14	AY413227	Homo sapi	
c 38	703.5	26.6	833	14	CB245337	UI-M_FAP1	
c 39	693	26.2	902	29	AY407184	Homo sapi	
c 40	691.5	26.2	2948	11	AK081344	Mus muscu	
c 41	686	26.0	902	29	AY407186	Mus muscu	
c 42	682.5	25.9	615	14	CB149460	KBEST0205	
c 43	679.5	25.7	1603	14	AY413229	Mus muscu	
c 44	672.5	25.5	1835	11	AK010496	Mus muscu	
c 45	666	25.2	1556	14	CD013895	CD013895	

#### ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	LINEAR
BG632919/c	BG632919	GH16126.3 prime GH Drosophila melanogaster head P02 Drosophila melanogaster cDNA clone GH16126.3 similar to CG4128; FBan004128	EST 23-APR-2001
		ion channel, located on: 2L 30D1-30E1; 04/10/2001, mRNA sequence.	
BG632919	BG632919		
		EST.	
		Drosophila melanogaster (fruit fly)	
		Drosophila melanogaster	
		Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	
		Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	

REFERENCE	Ephydrioidea; Drosophilidae; Drosophila.	
AUTHORS	1 (bases 1 to 885) Harvey, D., Brockstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G.M.	
TITLE	BDGP/HMW Drosophila EST Project	
JOURNAL	Unpublished (2001)	
COMMENT	Other Enrs: GH16126, 5prime Contact: Stapleton, M.	
FEATURES	BDGP Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: <a href="http://www.fruitfly.org/EST">http://www.fruitfly.org/EST</a> , est@fruitfly.berkeley.edu Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. hit genomic AE003511: arm:X [1879:641..191 3647] estimated cyto:18A3..18C6 [4/10/2001 Plate: GH.161 row: C column: 2 High quality sequence stop: 784. Location/Qualifiers	
source	1. .885 /organism="Drosophila melanogaster" /mol_type="mRNA" /db_xref="taxon:7227" /clone="GH16126" /sex="male and female" /dev_stage="adult" /lab_host="DHS - a alpha" /clone_lib="GH Drosophila melanogaster head pOT2" /note="Organ: head; Vector: pOT2; Site1: EcoRI; Site 2: XhoI; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."	
ORIGIN	US-09-303-232-6 (1-501) x BG632919 (1-885)	
Alignment Scores:		
Pred. No.:	54	Length: 885
Score:	1273.00	Matches: 227
Percent Similarity:	91.01%	Conservative: 26
Best Local Similarity:	81.65%	Mismatches: 25
Query Match:	48.22%	Indels: 0
DB:	12	Gaps: 0
Qy	LeuThrLeuGlnGinIleLeuAspValAspGluLysAsnGlnLeuIleLeuIleThrAsnIle 73	
Db	CTAACTATGAGATTATGATGTGACGAAGAAATCACTGCTTAAACGAAATT 826	
Qy	TriPheSerLeuGluTrpAsnAspGlyAsnLeuArgTrpAsnAspSerGluTyroGlyGly 93	
Db	TGGCTCAAATTGGATGGACGATGATGAACTCTCCATGGAAATTCTGGACTGGT 766	
Qy	ValIysAspLeuArgIleThrProAsnLysLeuTrpIlysProAspValLeuMetIysAsn 113	
Db	GTCGGGACTCGCAATTCTGGCACATGCTGCTTAAACGGGATGTTACTATGTAAC 706	
Qy	SerIleAspGluGlyPheAspGlyThrSerGlnIleAsnValVaValArgSerGlyGly 133	
Db	AGTGCACGCCGGGTTGATGGAACTGACGCCAAATAATGGTGTGGCAATAATGGG 646	
Qy	SerCysLeuIleProGlyIlePhenylserThrCysAspMetIyspheGlySerTrpThrTyrAspGlyAsn 173	
Db	TTTCATTCGAGATGATGAAATGGTCTCTGGACCTACATGGGTT 526	
Qy	GlnLeuAspLeuValLeuIlyAspGluAlaGlyGlyAspLeuSerAspPheIleThrAsn 193	
Db	CAGTGTGACCTGGCAATGTCAGGAACTGACGAACTGCTGTGGCACATTTACCTAACAT 466	

REFERENCE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
AUTHORS	Analysis of the mouse transcriptome based on functional annotation
TITLE	of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 184)
AUTHORS	Aizuchi,J., Aizawa,K., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Harara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoika,T., Hirozane,T., Horii,F., Imoto,K., Ishii,Y., Kondo,S., Konno,H., Kouda,M., Katoch,H., Kawai,J., Kohara,Y., Kondo,T., Miyazaki,A., Murata,M., Nishio,K., Nomura,K., Numazaki,R., Ohno,M., Obsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakatsume,N., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Tagabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Muramatsu,M. and Hayashizaki,Y.
TITLE	Submitted (16-JULY-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-rs@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: +81-45-503-9222, Fax: +81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://fantom.gsc.riken.go.jp/
FEATURES	Location/Qualifiers
source	<p>1. -1864          /organism="Mus musculus"          /mol_type="mRNA"          /strain="C57BL/6J"          /db_xref="FANTOM_DB:E130103E14"          /db_xref="MGI:2435288"          /clone="E130103E14"          /tissue type="eyeball"          /clone lib="RIKEN full-length enriched mouse cDNA library"          /dev_stage="0 day neonate"          /codon_start=1          /protein_id="BAC35404.1"          /db_xref="IGI:26343495"          /translation="MGVULPPPLSMILMLVMLPVASSEAHLRLPQLFEDNEYTEI          RPVANVSHPVVIIQFVEVSMSSQPVKVKDVEVNQMTENMLWKOINNDKLWKPSDQGVFB          MRPAAEKWPKDVIYNNADDFDVKDKTAKLKVTKGEVWMPAFLKSSKIDVTP          PFDYQONCTMPEFGWSYSDKAIDLDLVLIGSSNNLKDWSGEWAIAKPGYKHEIKYNNC          BEIQDQITLYIIRRPLFLFTNLICLPLSIFLTIVFLPSDCBEKVTLICIVSLL          LRVFLVIVITIPSLVLPVIGEVYLFTMLFVTSIVITYFLVNYHYRTPTHTMPT          WVKAVFLNLLPRVMENTRPTSEEDAPKTRNFYGAISLNCLNCFSRADSKSCKEGYPCQ          DGTGCVCHHRVKVNSFANSNTSSSESDAVLSALSPEIKEAQSIVXKAYNM          AQNVAKEIQQDWKVKYAMVIDFLWYFLVCLLGTAGLEQPLMARDDT"</p>
polyA_signal	1848 - 1853 /note="putative" 1864 /note="putative"
polyA_site	1864 - putative"
ORIGIN	303 Met Val AlaserServalValLeuAsnTyrHishiSArgTrAla 322
ALIGNMENT Scores:	1015 TTGTCACCTTGTCATCGTCATCAAGTCTTGCTCACGTCACAGAACACTCCG 1074
Pred. No. :	323 AspLeHiScluMetPrGlnTrPileLeuSerValPhelLeuProTrpPile 342
Score :	970.50 Length: 1864 Matches: 199

Db	1075	ACCAACAGATGCCACTGGGTCAAAGGCTGTGTTTGACCTTCCTCCAGGGTC 1134	PUBMED	11076661
QY	343	LeuArgMetSerArgProGlyLysIleThrArgLysThrIleMetMetAsnThrArg 362	REFERENCE	4
Db	1135	ATGTTATGACTGCCAACAGCAGGAAAGACGCCAAAGACAGGAATTCTAC 1194	AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
QY	363	MetArgGluIeuGlu-----LeuLysGluIuArgSerSerLeuLeuAla 378	TITLE	Functional annotation of a full-length mouse cDNA collection
Db	1195	GTTGTGAGTCTAACCTGAACCTGAACTGCTGCGACTCCANAGCTGC---- 1248	JOURNAL	Nature 409, 685-690 (2001)
QY	379	AsnValLeuAspIleAspaspAspPheArgHisGlyProProProAsnSerThrAla 398	REFERENCE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Db	1249	-----AAGGAAGCTAACCCCTGCAAGATGGACAGATGT 1281	AUTHORS	Authors of the mouse transcriptome based on functional annotation
QY	399	SerThrGlyAsnLeuGlyProGlyCysSerIlePheArg-----ThrAspPheArg 415	TITLE	Analysis of the mouse transcriptome of 60,770 full-length cDNAs (bases 1 to 2916)
Db	1282	GGCTAT-----TGCAACCACCGTAGGTAAAAATCTCAATTCTAGT 1323	JOURNAL	Nature 420, 563-573 (2002)
QY	416	ArgSerPheValArgProSerThrMetGluAspValGlyLys----GlyLeuGlySer 433	REFERENCE	6 (bases 1 to 2916)
Db	1324	GCCCARCTCAAGAAGCTCAAGCTCAAGCTGCTGAGTCGTCGCTGCTGCTGCT 1383	AUTHORS	Fukuda, S., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirose, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Koijima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Saito, R., Saito, H., Saitai, C., Saitai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, T., Toyota, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
Qy	434	HishisArgGluIleHiSLeuIleLeuArgGluLeuGlnPheIleAlaArgMetLys 453	TITLE	Direct Submission
Db	1384	CTGTCTACAGCAAGAAGCCATCAAAGTGAAAGTATATGCTGAAATAATGAA 1443	JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-303-9222, Fax: 81-45-503-9216)
Qy	454	LysAlaAspGluGluIleLeuIleSerAspTrpIysSheAlaAlaMetValValAsp 473	COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.
Db	1444	GCACAGATGTAGCCAAAGAGATTCAAAGATGTTGCAAGTGTGATTGAT 1503	URL	URL: http://genome.gsc.riken.go.jp/
QY	474	ArgPheCysLeuPheValPheThrIleLeuPheThrIleAlaThrValAlaValLeu 493	FEATURES	/Fantom3.gsc.riken.go.jp/.Location.Qualifiers
Db	1504	CGCATTTCTCTGGTTCTACCTCGTGTGCAATTAGGAAACGAGGATTATCTG 1563	COMMENT	1. -2916 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM DB: D130068A06" /db_xref="MGII:2420066" /db_xref="Itaxon:10090" /clone="D130068A06" /tissue_type="spinal ganglion" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="12 days embryo" 170. -1669 /note="unnamed protein product; NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR ALA8471, evidence: FASTY, 99.8% length, match=1497) putative" /codon_start=1 /protein_id="BAC34740.1" /db_xref="GI:26342156" /translation="MGMVLLPPPLSMMLVLMILPVVASASBAEHLFQQLFEDNNEITP RPVANTSHPVITIOFVMSMSOLVKDVNGOIMETNLWKLWPSKSDYCQEVEF MRVPARKIWRDIDVNAQDQFDKDTKQVDPYKQVQKQVQKQVQKQVQKQVQKQVQ PFDYQNCMTKPGSWYDKAQDIDLVGSSNNLKDYGEGVWLGKQVQKQVQKQVQKQVQ EEIYQDITSYLIRPLPFYTINLJIPCLLISLPLVFLPSDGEKVTLCLISV LTVFLVLTETIPTSLVPLGEVLYLPEIYUETLIVHYPPTHTMP WVKAVELNLPRVMEMTRPSTEADPKTFNFGYGBLSNINCFSRADSKEGKFCQ DGTCCYCHHRVKIENNSANTRSSSESDAVLSALSPEIKAQSYKTAEMK OKazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RESULT	3	AK051730	AK051730 2916 bp mRNA linear HTC 20-SEP-2003	CDS
LOCUS		Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone_D130068A06 product: NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.	FEATURES	
DEFINITION		AK051730 1 GI:26342155	SOURCE	
ACCESSION		HTC; CAP trapper.	ORGANISM	Mus musculus (house mouse)
VERSION		Mus musculus (house mouse)	KEYWORDS	Eukaryote; Metazoa; Chordata; Craniate; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
VERSION		1	ORGANISM	
VERSION		Carninci, P. and Hayashizaki, Y.	KEYWORDS	
VERSION		High-efficiency full-length cDNA cloning	ORGANISM	
KEYWORDS		Meth-Enzymol. 303, 19-44 (1999)	KEYWORDS	
KEYWORDS		992/9253	ORGANISM	
KEYWORDS		10309636	KEYWORDS	
KEYWORDS		110402159	KEYWORDS	
REFERENCE	2	Carinici, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	REFERENCE	Carninci, P., Itoh, M., Konno, H., Subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
AUTHORS		Genome Res. 10 (10), 1617-1630 (2000)	AUTHORS	Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL		20493374	JOURNAL	20493374
MEDLINE		110402159	MEDLINE	110402159
PUBMED			PUBMED	
REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akirama, J., Nishi, K., Kitsubiro, H., Kita, Y., Nakamura, S., Hazzama, M., Nishie, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuuwa, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.	REFERENCE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akirama, J., Nishi, K., Kitsubiro, H., Kita, Y., Nakamura, S., Hazzama, M., Nishie, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuuwa, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE		RIKEN integrated sequence analysis (RISA) system - 384-format sequencing pipeline with 384 multiplexillary sequencer	TITLE	RIKEN integrated sequence analysis (RISA) system - 384-format sequencing pipeline with 384 multiplexillary sequencer
JOURNAL		Genome Res. 10 (11), 1757-1771 (2000)	JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE		20530913	MEDLINE	20530913

/note="putative"

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kiria, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RIISA) system—384-format sequencing pipeline with 384 multipicropipette sequencer Genome Res. 10 (11), 1757-1771 (2000) MEDLINE 20530913 PUBMED 11076881

**REFERENCE 4**

TITLE The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

AUTHORS Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature

YEAR 409, 685-690 (2001)

**REFERENCE 5**

TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

AUTHORS Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature

YEAR 420, 563-573 (2002)

**REFERENCE 6** (bases 1 to 3126)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanasaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kouda, M., Katoh, H., Kawai, J., Koijima, Y., Kondo, S., Konno, H., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takakashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyoda, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

**REFERENCE 7**

TITLE Direct Submission

AUTHORS Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Biology, 2-1 Hirosawa, Wako, Saitama 351-0198, Japan

JOURNAL Submitted (16-APR-2002)

EXPLORATION Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

```

FEATURES          URL: http://genome.gsc.riken.go.jp/
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Db	968	ACGCTCTGCATCTCCCTGCTCTCCCTGACGGCTTCTCGTATACCGAGACC	1027	JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
QY	283	LeuProGlnValSerAspAlaIleProLeuLeuGlyThrTyrPheAsnCysIleMetPhe	302	COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
Db	1028	ATCCCTTCACAATGGTCACTCCCTGATCGGGAGTACCTCTCACTATGART	1087	FEATURES	Location/Qualifiers
QY	303	MetValAlaSerSerValValLeuThrValLeuAsnTyrHiShiSargThrAla	322	source	1..1436 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" <!...>1436 /gene="CHRNA3" /locus_tag="HCM1369"
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QY	343	LeuArgMetSerArgProGlyLysIleThrArgLysThrIleMetAsnThrArg	362	Alignment Scores:	
Db	1208	ATGTTATGACTAGGCCAAACAGCACGGAGAAGGCCAAAGAGGAACTTCTAC	1267	Pred. No.:	2.2e-101
QY	363	MetArgGluIleGlu-----LeuIysGluArgSerSerLysSerLeuLeuAla	378	Score:	957.50
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QY	379	AsnValLeuAspIleAspAspPheArgHisGlyProProProAsnSerThrAla	398	Best Local Similarity:	41.81%
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QY	416	ArgSerPheValArgProSerThrMetGluAspValGlyGly-----GlyLeuGlySer	433	Matches:	199
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QY	454	LysAlaAspGluGluIalLeuIleSerAspPheAlaAlaMetValValAsp	473	Gaps:	6
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LOCUS					
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ACCESSION		Homo sapiens CHRNA3 gene, VIRUAL TRANSCRIPT, partial sequence,			
VERSION		GI:39758856			
KEYWORDS		Genomic survey sequence.			
ORGANISM		Homo sapiens (human)			
TITLE		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.			
JOURNAL		Science 302 (5652), 1960-1963 (2003)			
REFERENCE		Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tarienbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.			
AUTHORS		Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			
PUBLISHED		1 ('bases 1 to 1436)			
REFERENCE	2 ('bases 1 to 1436)	Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tarienbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.			
AUTHORS		Direct Submission			
TITLE					
JOURNAL					
REFERENCE					
AUTHORS					
PUBLISHED					
REFERENCE					
AUTHORS					
TITLE					











Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Iishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Oneda, Y., Iishi, Y., Ozawa, K., Tanaka, T., Muramatsu, M., Inoue, Y., Okazaki, Y., Muramatsu, M., Matsui, A., Kawai, J., Kawai, J., RIKEN integrated sequence analysis system (RISA) system -384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE ID: 1020913

PUBMED ID: 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4037)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hirano, K., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kasukawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohssato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibaoka, A., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, K., Takahashi, F., Takaku, A., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

TITLE Submitted (16-JUL-2001) Yoshihiko Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome of RIKEN Yokohama Institute, RIKEN Genomic Sciences Center (GSC), Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT DNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to to prepare mouse tissues. Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/

Location/Qualifiers

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## ORIGIN

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Query Match:		34.49%	Indels: 55
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QY 61 AspValAspGluLySAsnGlnLeuLeuLeuThrAsnIleTrpLeuGluGluTrpAsn 80			
Db 404 AGGTGCMCGAGCGGAGATGACACCAACGCTGCTGACCTGAC 463			
QY 81 AspTYAsnLeuArgTrpAsnAspSerGluTrpGlyGlyValAspLeuArgIleThr 100			
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Db	1046 ATCTCCAAGATTTGTCCTCCACCTCCCTGACGTACCGCTGGAAAGTACCTCTATG 1105	REFERENCE AUTHORS 3 Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hara,K., Niesshine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,M., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A., and Hayashizaki,Y.
QY	299 CysIleMetTheMetValAlaSerSerValValLeuThrValValLeuLeuArgTrp 318	TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Db	1106 TTACCATGTCGTCAGTCCTCCATGCTACTGGTGTCTGTCAGTCAC 1165	JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
QY	319 HisArgThrAlaAspIleHisGluMetProGlnIlePheLeuGlnTrp 338	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium, Functional annotation of a full-length mouse cDNA collection
Db	1166 CACGGTTCGCTTACACGACCATGGGCCCTGGTCAAGCTGAACTGCTGGGC 1225	Nature 409, 685-690 (2001)
QY	339 LeuProTrpIleLeuArgMetSerArgProGlyLysIleThrArgLysThrIleMet 358	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Db	1226 CTGCCCACTCTCCCTCTTCCTGACGCCAGCCTGAACTGACGTCAC 1285	TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
QY	359 MetAsnThrArgMetArgGluLeuGluLeuLysGluArgSerSerLeuLeuIla 378	JOURNAL Nature 420, 563-573 (2002)
Db	1286 TTGGAAAGGGGCCAGGGAAACGTGAG-----GGGGCAGGCCACAPATTCC--- 1330	6 (bases 1 to 4046)
QY	379 AsnValLeuAspIleAspAspAspAspAspAspAspAspAspAspAspAspAsp 398	AUTHORS Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirao,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kasubawa,T., Katch,H., Kawai,J., Koijima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Saito,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shingayama,A., Shiraki,T., Sobagae,Y., Tagami,M., Tagawa,A., Takahashi,F., Tomaru,A., Takeda,Y., Tanaka,T., Tomaru,A., Toyota,T., Yasunishi,A., Muramatsu,M., and Hayashizaki,Y.
Db	1331 -----TTCGGCGAAGTCTGACCTGTCAGTCAGCTGACCTGC 1366	TITLE Direct Submission
QY	399 SerThrGlyAsnLeuGlyProGlyCysSerIlePheArgThrAspPheArgArgSerPhe 418	JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-303-9222, Fax: 81-45-303-9216)
Db	1367 -----TTT 1369	COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in RIKEN contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ . Location:Qualifiers
QY	419 ValArgProSerThrMetGluAspPheValGlyGly----- 429	1. 4046 /organism="Mus musculus" /mol_type="mRNA" /strain="IC57BL/6J" /db_xref="FANTOM DB:DBI300070121" /db_xref="MGI:1245010" /db_xref="taxon:10090" /clone="D130070121" /tissue_type="spinal ganglion" /clone_lib="RIKEN Full Length enriched mouse cDNA library" /dev_stage="12 days embryo" 209_1714 /note="unnamed protein product; cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal) (MGI:87891, GB NM_009602, evidence: BLASTN, 99%, match=1498) putative" /codon_start=1 /protein_id="PAC34749_1" /db_xref="NCI:26342174"
Db	1370 GTCATCTGATCATGCAAGGGCTTGACTGGCTTCCAGGGCTGAGGCCGCTGAGCC 1429	2 CDS
QY	430 GlyLeuLysSerIleSerGluLeuHisLeuIleLeuArgGlu-----Leu 445	3 Carninci,P., and Hayashizaki,Y.
Db	1430 GGTCMGGGGCTCGATGGGCCCATGCAAGCTGGTGGACGGTGTGG 1489	4 High efficiency full-length cDNA cloning
QY	446 GlnPheIleThrAlaArgMetLysIleAspPheGluAlaGluIleSerAspTP 465	5 Eukaryote; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Mus.
Db	1490 CGCTTATGGGACCATATGCAAGTGAAGATGATGACCA 1549	6 Enzymol. 303, 19-44 (1999)
QY	466 LysPheAlaAlaMetValAlaValAspArgPheCysLeuPheAlpThrLeuPheThrIle 485	7 99229253 1034636
Db	1550 AAATAGTTGCATGGTATGACCCCTGTCCTGCTGTC 1609	8 Carninci,P., and Hayashizaki,Y.
QY	486 IleLeuLysValAlaLeuLeu 493	9 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Db	1610 TTGGGACCATGGCATGTCCTG 1633	10 2049974 11042159
RESULT 11	AK051742	1 Carninci,P., and Hayashizaki,Y.
LOCUS	AK051742	2 Carninci,P., and Hayashizaki,Y.
DEFINITION	4046 bp mRNA linear HTC 20-SEP-2003	3 High efficiency full-length cDNA cloning
ACCESSION	AK051742	4 Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130070121 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence.
VERSION	AK051742.1	5 Eukaryote; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Mus.
KEYWORDS	GI:26342173	6 Mus musculus (house mouse)
ORGANISM	Mus musculus	7 Eukaryote; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Mus.
JOURNAL		8 Carninci,P., and Hayashizaki,Y.
MEDLINE		9 Carninci,P., and Hayashizaki,Y.
PUBLMED		10 2049974 11042159
REFERENCE		1 Carninci,P., and Hayashizaki,Y.
AUTHORS		2 Carninci,P., and Hayashizaki,Y.
TITLE		3 High efficiency full-length cDNA cloning
JOURNAL		4 Mus musculus
MEDLINE		5 Eukaryote; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Mus.
PUBLMED		6 Carninci,P., and Hayashizaki,Y.
REFERENCE		7 Carninci,P., and Hayashizaki,Y.
AUTHORS		8 Carninci,P., and Hayashizaki,Y.
TITLE		9 Carninci,P., and Hayashizaki,Y.
JOURNAL		10 2049974 11042159
MEDLINE		11 Carninci,P., and Hayashizaki,Y.
PUBLMED		12 Carninci,P., and Hayashizaki,Y.

ORIGIN		Alignment Scores:		US-09-303-232-6 (1-501) x AK051742 (1-4046)					
Pred.	No.:	Length:	4046						
Qy	23	GluLysArgLeuAsnAlaLeu-----AlaAsnTyrAsnThrLeuGluArgPro	4.31e-95	Score:	910.50	Matches:	185		
Db	293	GAGGAAGCCTGGAGCATTCATGGATCCCTCCGCCTATAACAAAGCTGATCCGTC	57.38%	Percent Similarity:	95	Conservative:	95		
Qy	41	ValAlaAsnGluserGluProLeuGluValAlaArgPheGlyLeuThrIeuGlnGlnLeile	37.91%	Best Local Similarity:	153	Mismatches:	153		
Query Match:			34.49%	DB:	11	Indels:	55		
Qy	61	AspTyrAsnLeuArgTrpAsnAspSerGluTyrglylyvallysAspLeuArgIleThr	11	Gaps:	9				
Db	413	AGTGTGCAGAGCGGGAGCATGACCACCAACCTCTGCTGACCCAGAGTGCGAA	80						
Qy	81	AspTyrAsnLeuArgTrpAsnAspSerGluTyrglylyvallysAspLeuArgIleThr	100						
Db	473	GATTATCCCTCACATSGAAGCTGAGTTGACATATGAGAAAGTCGACICCT	100						
Qy	101	ProAsnLysLeuTrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAsp	120						
Db	533	TCTAAAGACATCTGGCTCCAATGCGCTCTATGACAATGTCGACGGCATGPA	592						
Qy	121	GlyThrThrGlnThrAsnValValAlaArgSerGlyGlySerCysLeutYrValProPro	140						
Db	593	GTCCTCTCTATTCATGCTGCTCTCCATGATGCGCATCTTGGCTACGCC	652						
Qy	141	GlyIleIleSerThrCysLysMeAspIleAspLeuAlaTrpPheProPheAspGlnHis	160						
Db	653	GCCATCUPACAAGGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCA	772						
Qy	161	CysAspMetLysPheGlySerIrrpThrTyrAspGlyAsnGlnLeuAspIeuValLeuLys	180						
Db	713	TGGCACCATGAGATTCCCTCTGGACTTACACGGACTASGAGTACCTGGTGTCAA	180						
Qy	181	AspGluAlaGlyGlyAspIeuUserAspPheIleThrAspGlyGluTyrLeuIleGly	200						
Db	773	AGCGAATGTG--GCCAACCTGAGCAGCTTACACCTAGTCCGGACTGGACATCGCA	829						
Qy	201	MetProGlyLysLysSerThrIleThrTyrAlaCysProGlu-----ProTyrVal	218						
Db	830	CTGGCAAGCCGCAACGCCATGCCATGCCATGCCATGCCATGCCATGCCA	238						
Qy	219	AspValThrPheThrIleMetLeuGlyArgArgThrLeuTyrTyrPheAspLeuLeu	238						
Db	875	GACATGACCTGACTCATATTCTCGAAACCGCTCTACACCATCAACCTCATC	934						
Qy	239	ValProCysValLeuLeuSerSerMetAlaLeuIleGlyDipeptLeuProAspSer	258						
Db	935	ATCCCTCGCTGACTCTACACTCGCTGGCCATACCTGCTCTACCTGCTCTAGA	994						
Qy	259	GlyGluLysLeuThrLeuGlyValThrIleLeuSerLeuThrValPheLeuAsnLeu	278						
Db	995	GGTGAAGAGTAGCAGCTTCTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1054						

Qy	279	ValAlaGluThrLeuProGlnValAsparAspAlaIleProLeuLeuGlyThrGlyThrTyrPheAsn	298
Db	1055	ATCTCCAGATGTGGCTCCCCACCTCTCTCAGPACCGCTGGAAAGTACCTCATG	1114
Qy	299	CysIleMetPheMetValAlaSerSerValLeuThrValAlaValLeuAsnThrHis	318
Db	1115	TTCACCATGGTGCTAGCACCTTCATCTCACTAGCGGTGTCATGGCAC	1174
Qy	319	HisArgThrAlaAspIleHisGluMetProGlnTrpIleLysSerValAlaLeuGlnTrp	338
Db	11175	CACCGCTACACGCAACATGGCCAGGCTAACGGCTAGGTGAAAGGTGTCATGGCAC	1234
Qy	339	IeuProTrpIleLeuArgMetSerArgProGlyLysIleIleArgLysThrIleMet	358
Db	1.235	CTGCCAACCTTCCTCTCCAGAAGCCACGCCAACGCTGACTGACGCTGC	1294
Qy	359	MetAspIleArgMetArgGluLeuLysGluArgSerSerLysSerIleLeuAla	378
Db	1295	TTCGAAGGGCCACGGGAACTGGAAAGCTGAACTGCTGAG	1339
Qy	379	AsnValLeuAspIleAspAspAspPheArgGlyGlyProProProAsnSerThrAla	398
Db	1340	TTCCCGAAAGTCCGACGTGACCTGACGTCATGACCTGAC	1375
Qy	399	SerThrGlyAsnLeuGlyProGlyCysSerIlePheArgThrAspPheArgSerPhe	418
Db	1376	-	1378
Qy	419	ValArgProSerThrMetGluAspValGlyGly-----	429
Db	1379	GTCATTCCTGCATAATTGAGGGCTGATGGCTGGGCTCTTCAGGTGAGGCCGTCAGGCC	1438
Qy	430	GlyIeuGlySerHisIshargGluLeuHisLeuIleLeuArgGlu-----	445
Db	1439	GGTCTGGGGGCTGATGGGCCATGACCTGTCGCTCCGGAAAGTGTGGACGGTGG	1498
Qy	446	GlnPheIleIleIleArgMetLysLysAlaaspGluGluAlaIleLeuIleSerAspTrp	465
Db	1499	CGCTCTCATGGGCCACCATGGAAAGTGAAGATGATGACCAAGTGTGAGGAGATGG	1558
Qy	466	LysPheAlaAlaIleMetValAlaValAspArgPheCysIleuPheValPheThrIle	485
Db	1559	AAATACGTGCCATGGTATGACCGCCGTTCTCTGGATCTTGTCTGTC	1618
Qy	486	IleAlaThrValAlaValLeuIle	493
Db	1619	TTGGGACCATGGCATTCCTG	1642
RESULT	12		
AL530299		1201 bp mRNA linear EST 23-MAY-2003	
LOCUS		Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens	
DEFINITION		CDNA clone CSOPD00YF05 5'-PRIME, mRNA sequence.	
ACCESSION		AL530299	
VERSION		AL530299.2	
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
REFERENCE		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		Li, W.B., Gruber, C., Jesse, J., and Polayes, D.	
TITLE		Full-length cDNA libraries and normalization	
JOURNAL		Unpublished (2001)	
COMMENT		On Feb 13, 2001 this sequence version replaced gi:12793792.	
Contact:	Genoscope		
Genoscope - Centre National de Séquençage			
BP 191 91006 EVRY cedex - France			
Email: segr@genoscope.cns.fr			
was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7646. x For more information about this cluster, see			

cgi-bin/cluster.cgi?seq=CSODD007CH03QPI&cluster=7646.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CSODD007CH03QPI.  
 Location/Qualifiers  
 1. .1201  
 source  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone=CSODD007YPOS1  
 /tissue\_type="NEUROBLASTOMA COT 50-NORMALIZED"  
 /clone\_id="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI oligo (GT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."



Db	1040	GGCGGTACTGCTTACCAAGATCTCGTACCCCTCGATTGTCAAGGTCTTC	1099
QY	314	ValLeuAsnTyRHisIargThrAlaAspLeuIgluMetProGlnIrrpIleYssEr	333
Db	1100	GTGCTTAATGTTACACCGCTCACACGCAACACACCATGCCACACACCACGAGA	1159
QY	334	ValPheLeuGlnIrrpIleLeuIrrpIleLeuArgIleSerArgProGly-----LysLys	351

Db	1160	GCCTTCCTGGACATTGTCGCCCTCATGAGGCCCATCTGGTCAAAGAC	1219	REFERENCE AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Qy	352	IleThrAlaGlyThrIleMetMetAsnThrArgMetAlaGluLeu-----	368	TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Db	1220	AACTCGCGAGACTATCCGAATCCATGCAAAAGATGGCCACGCCCTCGTTCTGGC-C	1279	JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
Qy	369	LysGluIarsserLysserLeuLeuIasnValLeuAsp-----	382	MEDLINE	20493374
Db	1280	GAGCTGTAGTGAGCCGGCATTGCTGACCTGGTACATGGCTGACCTGCG	1339	PUBLMED	11042159
Qy	383	-----IleAsp---AspAspPheArgIsglyProPr-----	392	REFERENCE AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, M., Hazama, M., Nishime, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, A., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishii, T., Tanaka, T., Matsutera, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
Db	1340	CCAACTTTGCAACCAGATGGCACAGGAGTCGAGACCAGCTACATGAGTCACC	1399	TITLE	RIKEN integrated sequence analysis (RISA) system -384-format sequencing pipeline with 384 multiplexillary sequencer
Qy	392	OPOProtranser-----	396	JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
Db	1400	TCCCCACAAGGTCCCTGACTTGAGAACATAGAGGTTGAGAAGGCCAGTCCCCTGATCA	1459	MEDLINE	20530313
Qy	396	-----	396	PUBLMED	11078661
Db	1460	CCTGGCTCTGTGACCCACCAAATAGCAGTAGCCCATGGGCCCCAGTGCATCAAAGCAGGTC	1519	REFERENCE AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Qy	397	-----ThrAlaSerThrGlyAs-----	402	TITLE	Functional annotation of a full-length mouse cDNA collection
Db	1520	CTGAGCGTCAGATGTGCCAGTCCAGGAGCAGCGGAGGATccTGCCTGCCG	1579	JOURNAL	Nature 409, 685-690 (2001)
Qy	402	neuGlyProGlycSerSerIlePheArgThrAspArgSerPheVal-----	419	REFERENCE AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Db	1580	TCTCGGAGTATGCAAGTCACTGTTCC-CAAAGATGGAGCTGCTCCAGACTGAGGCAA	1638	TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Qy	419	-----	419	JOURNAL	Nature 420, 563-573 (2002)
Db	1639	GCCCCACTGGCTCCAGGCTCCCTGAAGBCCCCCTCATGCCAGTTGTCAGCCA	1698	PUBLMED	6 (bases 1 to 3230)
Qy	420	-----ArgProserThrMetGluAspVal-----	427	REFERENCE AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoaka, T., Hizozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, H., Kouda, M., Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Onstot, N., Okazaki, Y., Saito, R., Saitoh, R., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibaoka, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Db	1699	GACTCTCATGCAATGGACATGCAAGAACCATCTCTGTCCCCTCATCTGCT	1758	TITLE	Direct Submission
Qy	428	----GlyGlyGlyIleGlyGlySerHshiIargGluLeuHisLeu-----	440	JOURNAL	Submitted (16/Apr/2002) Yoshihiko Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp, Tel: +81-45-503-9222, Fax: +81-45-503-2126)
Db	1759	CAAGGCTGGAGCCACCAAGGCCACCTCCCACACTGCTGACAGCAG	1818	COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedi Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.
Qy	441	-IleLeuArgGluLeuGlnPheIleAlaArgMetlysLysAlaArgGluAlaGlu-----	460	FEATURES	URL: http://genome.gsc.riken.go.jp/
Db	1819	GCGAGTAAGGGACTCCATTACATGGAGAACCTCAGGGAGAAGAACACTCTC	1878	source	URL: http://fantom.gsc.riken.go.jp/
Qy	460	LeuIleLesserAspTrpIleSpheAlaAlaMetAlaValAspArgHecysLeuIpheValPh	480		
Db	1879	GFTGAAGGGGACTGGAAATACGTGGCCATTGGCATTCCTCTCTGGATSTT	1938		
Qy	480	493-----ethrLeuIpheThrIleAlaIthrValAlaLeuLeu-----	493		
Db	1939	CATATTGTGCTTCGGACTGTGGACTCTTCCCTG	1978		
RESULT	15				
LOCUS	AK083157				
DEFINITION	Mus musculus adult male hippocampus CDNA, RIKEN full-length enriched library, clone: c63019M18 product: cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.				
ACCESSION	AK083157				
VERSION	AK083157.1				
KEYWORDS	HTC, CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
Bukaryota:	Metazoia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.				
REFERENCE	Carninci, P. and Hayashizaki, Y.				
AUTHORS	High-efficiency full-length cDNA cloning				
JOURNAL	High-mol. weight Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBLMED	10349636				



Db 1739 GGCAGTAGAAGGGTCCAGTAGTCATTGAGGACACCTAAGGAGAAGACAGACTCTC 1798  
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Db 1799 GTGAAAGGGACTGGATAACCTGGCATGGTCATGGCATCGAGATCTCTGGGTT 1858  
Qy 480 erThrLeuPheThrIleAlaIleAlaIleAlaIleAlaValAlaValLeu 493  
Db 1859 CATCATCTGCCTTCGGCACTGGCACTGGCACTGGCACTTCCTG 1898

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